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From: Saidha, Tekchand  
Sent: Tuesday, March 04, 2003 4:00 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/017145 - sequence search request

**10/017145** - sequence search request

Please search the data bases and Interference files for :

SEQ ID NO : 1

Thank you,

*Tekchand Saidha*  
*Primary Examiner*  
*Art Unit 1652, CM1, Room No. 10D05*  
*Mail Box 10D01*  
*(703) 305-6595*

RECEIVED  
MAR - 4 2003  
STIC/BIOTECH. DIVISION  
(STIC)

Point of Contact  
P. Sheppard  
Telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 3/7/03  
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Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:06:42 ; Search time 33 seconds  
(without alignments)  
2266.518 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKSQSEVENLKKPFMP.....RAKEAPMPFWIFDRQVKL 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1771	92.4	396	10 Q43140	Q43140 sesamum ind
2	1757	91.7	396	10 Q43141	Q43141 sesamum ind
3	1746	91.1	396	10 Q93X20	Q93X20 sesamum ind
4	1733	90.4	401	10 Q22832	Q22832 arabidopsis
5	1729	90.2	401	10 Q94AE9	Q94AE9 arabidopsis
6	1727	90.1	396	10 Q24497	Q24497 helianthus
7	1701	88.8	396	10 Q24498	Q24498 helianthus
8	1698	88.6	396	10 Q9SEK6	Q9SEK6 persea amer
9	1698	88.6	401	10 Q39355	Q39355 brassica na
10	1696.5	88.5	409	10 Q9SW87	Q9SW87 arachis hyp
11	1695	88.5	401	8 Q9XOR7	Q9XOR7 brassica ju
12	1688	88.1	396	10 Q65040	Q65040 macfadyena
13	1673	87.3	396	10 Q8VXJ7	Q8VXJ7 helianthus
14	1670	87.2	396	10 Q8VXJ8	Q8VXJ8 helianthus
15	1660.5	86.7	407	10 Q42591	Q42591 arabidopsis
16	1653.5	86.3	396	10 Q8S059	Q8S059 oryza sativ

17	1652	86.2	358	10 Q43196	Q43196 thunbergia
18	1637	85.4	396	10 Q9M4N5	Q9M4N5 gossypium h
19	1629	85.0	396	10 Q82014	Q82014 linum usita
20	1620	84.6	396	10 Q9SBA2	Q9SBA2 linum usita
21	1608	83.9	399	10 Q947F1	Q947F1 kochia scop
22	1601	83.6	390	10 Q43197	Q43197 thunbergia
23	1600.5	83.5	396	10 Q9M879	Q9M879 arabidopsis
24	1599	83.5	390	10 Q43198	Q43198 thunbergia
25	1526.5	79.7	394	10 Q9LF04	Q9LF04 arabidopsis
26	1405.5	73.4	386	10 Q947F2	Q947F2 kochia scop
27	1380	72.0	411	10 Q9M881	Q9M881 arabidopsis
28	1358	70.9	401	10 Q9LF05	Q9LF05 arabidopsis
29	1351	70.5	396	10 Q9M880	Q9M880 arabidopsis
30	1318	68.8	374	10 Q9MAR6	Q9MAR6 arabidopsis
31	1315	68.6	384	10 Q9XFC1	Q9XFC1 lupinus lut
32	1261	65.8	387	10 Q41510	Q41510 thunbergia
33	1219.5	63.6	385	10 P92933	P92933 asclepias s
34	1218	63.6	368	10 Q40879	Q40879 pelargonium
35	1009.5	52.7	222	10 Q64906	Q64906 pelargonium
36	771	40.2	167	10 Q43142	Q43142 sesamum ind
37	745	38.9	161	10 Q9XEH1	Q9XEH1 elaeis guin
38	307	16.0	328	16 Q9XAL3	Q9XAL3 streptomyce
39	272	14.2	338	16 Q8VKD4	Q8VKD4 mycobacteri
40	272	14.2	338	16 Q50824	Q50824 mycobacteri
41	267	13.9	338	16 Q50050	Q50050 mycobacteri
42	158	8.2	275	16 Q9X793	Q9X793 mycobacteri
43	142	7.4	170	2 Q9K539	Q9K539 mycobacteri
44	138	7.2	275	16 Q53442	Q53442 mycobacteri
45	126.5	6.6	1349	5 Q9VPR5	Q9VPR5 drosophila

#### ALIGNMENTS

RESULT 1

Q43140 ID Q43140 PRELIMINARY: PRT; 396 AA.  
AC Q43140;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Acyl-[acyl-carrier protein] desaturase precursor (EC 1.14.99.6)  
DE (Stearoyl-ACP desaturase).  
OS Sesamum indicum (Oriental sesame) (Gingelly).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.  
OX NCBI\_TaxID=4182;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=4294;  
RX MEDLINE=96213006; PubMed=8665096;  
RA Yukawa Y., Takaiwa F., Shoji K., Masuda K., Yamada K.;  
RT "Structure and expression of two seed-specific cDNA clones encoding  
RT stearoyl-acyl carrier protein desaturase from sesame, Sesamum indicum  
L.";  
RL Plant Cell Physiol. 37:201-205(1996)  
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A  
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL  
CC CHAIN (BY SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)  
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.  
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY  
CC SIMILARITY).  
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY  
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE  
CC OILS.  
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
DR EMBL: D42086; BAA07681.1; -;  
DR HSSP: P22337; IAFR.  
DR InterPro: IPR005067; FA\_desat.

DR InterPro: IPR001225; FA\_desaturase.  
 DR Pfam: PF03405; FA\_desaturase-2; 1.  
 DR PROSITE: PS00574; FATTY-ACID-DESATUR\_2; 1.  
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;  
 FT TRANSIT peptide.  
 FT CHAIN 1 33 POTENTIAL.  
 FT CHAIN 34 396 STEAROYL-ACYL CARRIER PROTEIN DESATURASE.  
 SQ SEQUENCE 396 AA: 45168 MW: 423475AB676A0940 CRC64;  
 Query Match 92.4%; Score 1771; DB 10; Length 396;  
 Best Local Similarity 91.2%; Pred. No. 7.6e-137;  
 Matches 331; Conservative 20; Mismatches 12; Indels 0; Gaps 0;

QY 1 ASTLKSSEVENLKKPFPPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVK 60  
 DB 34 ASTLRSGSEVETVKKPFPPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVK 93  
 QY 61 CWQPDPLDPASDGDGEQVRELRLRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120  
 DB 94 CWQPDPLDPSSDGDGDQVKELRLRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153  
 QY 121 VRDETGAAPTSMWAIWTRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180  
 DB 154 VRDETGAAPTSMWAIWTRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 213  
 QY 181 TENSPLYGFTYTFQERATFISHGNTARAKHEGDIKLAQICGTIAADEKRKHETAYTKIV 240  
 DB 214 TENSPLYGFTYTFQERATFISHGNTARAKHEGDIKLAQICGTIAADEKRKHETAYTKIV 273  
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRGLGVYAKDYADI 300  
 DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRGLGVYAKDYADI 333  
 QY 301 LEFLVGRWKVDKLTGLSAGQKADYVCRPLPRIRLEERAQRAKEAPMPFSWIFDRQ 360  
 DB 334 LEHLVARKVKNLTGLSADGRKADYVCGPLPRIRLEERAQRAKEAPMPFSWIFDRQ 393  
 QY 361 VKL 363  
 DB 394 VQL 396

RESULT 2  
 Q43141 ID Q43141 PRELIMINARY; PRT; 396 AA.  
 AC Q43141  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).  
 DE Sesamum indicum (Oriental sesame) (Gingelly).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.  
 OX NCBI\_TaxID=4182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=4294;  
 RA Yukawa Y., Takaiwa F., Yamada K.;  
 RT "Structure and expression of two cDNA clones encoding stearoyl-acyl carrier protein desaturase in sesame."  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.  
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).  
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
 DR EMBL: D49832; BAA08635.1; -;  
 DR HSP; P22337; IAFR.  
 DR InterPro: IPR005067; FA\_desat.  
 DR InterPro: IPR001225; FA\_desaturase.  
 DR Pfam: PF03405; FA\_desaturase-2; 1.  
 DR PROSITE: PS00574; FATTY-ACID-DESATUR\_2; 1.  
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;  
 KW Transit peptide.  
 SQ SEQUENCE 396 AA: 45212 MW: 1335DEC4A1B2BF9A CRC64;  
 Query Match 91.7%; Score 1757; DB 10; Length 396;  
 Best Local Similarity 90.6%; Pred. No. 1.1e-135;  
 Matches 329; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 ASTLKSSEVENLKKPFPPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVK 60  
 DB 34 ASTLRSGSEVETVKKPFPPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVK 93  
 QY 61 CWQPDPLDPASDGDGEQVRELRLRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120  
 DB 94 CWQPDPLDPSSDGDGDQVKELRLRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153  
 QY 121 VRDETGAAPTSMWAIWTRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180  
 DB 154 VRDETGAAPTSMWAIWTRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 213  
 QY 181 TENSPLYGFTYTFQERATFISHGNTARAKHEGDIKLAQICGTIAADEKRKHETAYTKIV 240  
 DB 214 TENSPLYGFTYTFQERATFISHGNTARAKHEGDIKLAQICGTIAADEKRKHETAYTKIV 273  
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRGLGVYAKDYADI 300  
 DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRGLGVYAKDYADI 333  
 QY 301 LEFLVGRWKVDKLTGLSAGQKADYVCRPLPRIRLEERAQRAKEAPMPFSWIFDRQ 360  
 DB 334 LEHLVARKVKNLTGLSADGRKADYVCGPLPRIRLEERAQRAKEAPMPFSWIFDRQ 393  
 QY 361 VKL 363  
 DB 394 VQL 396

RESULT 3  
 Q93X20 ID Q93X20 PRELIMINARY; PRT; 396 AA.  
 AC Q93X20  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Stearoyl acyl carrier protein.  
 OS Sesamum indicum (Oriental sesame) (Gingelly).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.  
 OX NCBI\_TaxID=4182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=DEVELOPING SEED;  
 RA Kanrar S.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=DEVELOPING SEED;  
 RA Chopra V.L.;  
 RT "transgenic expression of cDNA encoding steroyl acyl carrier protein desaturase of sesamum indicum in Indian mustard."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.

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RC TISSUE=DEVELOPING SEED;
RA Chopra V.L.;
RT "Trangenic indian mustard high in oleate.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ313331; CAC44792.1; -.
DR InterPro: IPR005067; FA_desat.
DR Pfam: PF03405; FA_desaturase.2; 1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; UNKNOWN1.
SQ SEQUENCE 396 AA; 45054 MW; 4945DFAC6687BEB2 CRC64;

Query Match 91.1%; Score 1746; DB 10; Length 396;
Best Local Similarity 89.8%; Pred. No. 8.5e-135;
Matches 326; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 1 ASTLKSQKEVENLKKPMPREHVQVTHSMPPQKIEFKSLDWAENILVHLKPVKEK 60
DB 34 ASTLSSGKEVETVKRPNPREHVQVTHSMPPQKIEFKALDWAENILVHLKPVKEK 93
QY 61 CWQPDPLDPASDGFQVRELREAKEIPDDYFVLVGDMDITEALPTQTMNTLDG 120
DB 94 CWQPDPLDPSSDGFQVRELREAKEIPDDYFVLVGDMDITEALPTQTMNTLDG 153
QY 121 VRDETGAAPTSAIWTAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYLGSGMDPR 180
DB 154 VRDETGAAPTSAIWTAWTAENRHGDLNKKLYLSGRVDMRPNKGFYRLIGSGMDPR 213
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDILKLAQICGTTAADEKRHETAYTKIV 240
DB 214 TENSPLYGFIYTSFOERATFISHGNTARLAREHGDILKLAQICGTTAADEKRHETAYTKIV 273
QY 241 EKLFEIDPDGTVLAFADMMRKKSIPAHLMVDGRDNLDFHFSAVAQRLGVYTKADYADI 300
DB 274 EKLFEIDPDVTVLAFADMMRKKSIPAHLMVDGRDNLDFHFSVAQRLGVYTKADYADI 333
QY 301 LEFLVGRWKVDKLTGLSAGQKAQDYVCLRPRIIRLEERAQGRAKEAPTMPSWIFDRQ 360
DB 334 LEHLVARNKVNLTGLSADGQKAQDYVCGLPRIIRLEERAQGRAKAPKIPFSWVHRE 393
QY 361 VKL 363
DB 394 VOL 396

RESULT 4
Q22832
ID O22832 PRELIMINARY; PRT; 401 AA.
AC O22832;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP
DE desaturase).
GN AT2G43710 OR SS12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=21374454; PubMed=11481500;
RA Kachroo P., Shanklin J., Shah J., Whittle E.J., Klessig D.F.;
RT "A fatty acid desaturase modulates the activation of defense signaling
RT pathways in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9448-9453(2001).
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: AC002333; AAB64035.1; -.
DR EMBL: AF395441; AAK85232.1; -.
DR HSP; P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase.2; 1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 401 AA; 45693 MW; 0C46984578D4E1D1 CRC64;

Query Match 90.4%; Score 1733; DB 10; Length 401;
Best Local Similarity 89.4%; Pred. No. 1e-133;
Matches 322; Conservative 22; Mismatches 16; Indels 0; Gaps 0;

QY 4 LKSGSKEVENLKKPMPREHVQVTHSMPPQKIEFKSLDWAENILVHLKPVKEKWQ 63
DB 42 LSSGPKVESEVSKKPTPPREHVQVTHSMPPQKIEFKSMENWAEENLILHLKDVEKSWQ 101
QY 64 PODELPDPASDGFQVRELREAKEIPDDYFVLVGDMDITEALPTQTMNTLDGVRD 123
DB 102 PODELPDPASDGFQVRELREAKEIPDDYFVLVGDMDITEALPTQTMNTLDGVRD 161
QY 124 ETGASPTSAIWTAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYLGSGMDPRTEN 183
DB 162 ETGASPTSAIWTAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYLGSGMDPRTEN 221
QY 184 SYPLGFIYTSFOERATFISHGNTARQAKEHGDILKLAQICGTTAADEKRHETAYTKIVEKL 243
DB 222 NPYLGIYTSFOERATFISHGNTARQAKEHGDILKLAQICGTTAADEKRHETAYTKIVEKL 281
QY 244 FEIDPDGTVLAFADMMRKKSIPAHLMVDGRDNLDFHFSAVAQRLGVYTKADYADILEF 303
DB 282 FEIDPDGTVMFAFADMMRKKSIPAHLMVDGRDNLDFNFSVAQRLGVYTKADYADILEF 341
QY 304 LVGRWKVDKLTGLSAGQKAQDYVCLRPRIIRLEERAQGRAKEAPTMPSWIFDRQVKL 363
DB 342 LVGRWKIQDILTGLSGENKAQDYVCLGAPRIKRLDERAQAQAKKPKIPFSWIHREVQL 401

RESULT 5
Q94AE9
ID Q94AE9 PRELIMINARY; PRT; 401 AA.
AC Q94AE9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE AT2G43710/F18019.18.
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OS Arabidopsis thaliana (Mouse-ear-cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OC NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,  
RA Koesema E., Chen H., Carninci P., Dale J.M., Gibson H.A.,  
RA Banh J., Bowser L., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,  
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J.,  
RA Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,  
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,  
RA Davis R.W., Theologis A., Ecker J.R.;  
RA "Arabidopsis cDNA clones.";  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,  
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,  
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,  
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,  
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,  
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,  
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
RA Ecker J.R.;  
RT "Arabidopsis ORF clones.";  
RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY048233; AAK82496.1; -;  
DR EMBL: AY094014; AAM16170.1; -;  
DR InterPro: IPR005067; FA.desat.  
-DR InterPro: IPR001225; FA.desaturase.  
DR InterPro: PF03405; FA.desaturase.2; 1.  
DR PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; UNKNOWN\_1.  
DR SEQUENCE 401 AA; 45692 MW; 01F09DD370F4E1D1 CRC64;  
SO

Query Match	90.24%	Score 1729;	DB 10;	Length 401;
Best Local Similarity	89.24%	Pred. No. 2.2e-133;		
Matches 321;	Conservative 23;	Mismatches 16;	Indels 0;	Gaps 0;

Qy	4	LKSGSKEVENLKKPMPREHVQVTHSMPPQKTEIFKSLDNWAFENILVHLKPVEKQW	63
Db	42	LSSGPKVESLKKPTPPREHVQVHLHSMPPQKTEIFKSMENWAEENLIHLKDVESKWQ	101
Qy	64	PODFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYTQTMNLTDGVRD	123
Db	102	PODFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYTQTMNLTDGVRD	161
Qy	124	ETGASPTSWAIWTRAWTAENRHGDLNLNKLYLSGRVDMRQIEKTIQYLGSGMDPRTE	183
Db	162	ETGASPTSWAIWTRAWTAENRHGDLNLNKLYLSGRVDMRQIEKTIQYLGSGMDPRTE	221
Qy	184	SPYLGFIYTSFOERATFTISHGNTARQAQKEHGDIKLAQICGTIAADEKRRHETAYTKIVEKL	243
Db	222	NPYLGFIYTSFOERATFTISHGNTARQAQKEHGDIKLAQICGTIAADEKRRHETAYTKIVEKL	281
Qy	244	FEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYVYAKDYADILEF	303
Db	282	FEIDPDGTVMFADMMRKKISMPAHLMYDGRDNLDFNFSVAQRLGVYVYAKDYADILEF	341
Qy	304	LVGRKWKVKLTGLSREGOKAQDYVCRLLPPIRRLERAAQGRAKEAPTWPFSWIFDQVKL	363
Db	342	LVGRWKIKQDLTGLSGEGNKAQDYLCGLAPRIKRLDERAAQARKGPKIPFWSIHDREVOL	401

RESULT 6		
O24497	PRELIMINARY:	PRT: 396 AA.
ID	O24497	
AC	O24497;	
DT	01-JAN-1998 (TREMBLrel. 05, Created)	
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	

DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP  
DE desaturase).  
DE Helianthus annuus (Common sunflower).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;  
OC Heliantheae; Helianthus.  
OC NCBI\_TaxID=4232;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=MAMMOTH;  
RC Hongtrakul V., Slabaugh M.B., Knapp S.J.;  
RA "Sunflower stearoyl-ACP desaturase.";  
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
RL -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A  
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACRYL  
CC CHAIN (BY SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)  
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.  
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY  
CC SIMILARITY).  
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY  
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE  
CC OILS.  
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
DR EMBL; U91339; AB65144.1; -.  
DR HSPS; P22337; IAFR.  
DR InterPro; IPR005067; FA\_desat.  
DR InterPro; IPR001225; FA\_desaturase.  
DR Pfam; PF034405; FA\_desaturase\_2; 1.  
DR PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
DR Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;  
KW Transit peptide.  
SQ SEQUENCE 396 AA; 45128 MW; BC79CA9631952E11 CRC64; 1;

	Query Match	90.1%	Score 1727;	DB 10;	Length 396;	
	Best Local Similarity	88.7%;	Pred. No. 3.le-133;			
	Matches 32;	Conservative	23;	Mismatches 18;	Indels 0;	Gaps 0;
Qy	1	ASTLKSKEVENLKPPMPPREVHVQTHSMPPQKIEIFKSLDNWAENTILVLHLKPVEK	60			
Dd	34	ASTIGSTPKVESTKKPTTPREVHLQVTHSMPPQKIEIFKSGAEDNLLVLHLKPVEK	93			
Qy	61	CWQPQDLPLDPASDGFDFSOVELRERAKEIPDDYFVVVLGDMITEALPTYOTMLNTLDG	120			
Dd	94	CWQPQDLFLPASDGFSEQVKELRAKEIIDEYFVVVLGDMITEALPTYOTMLNTLDG	153			
Qy	121	VREDTGASPTSWAIWTRAWTAENRHGDLLNKLYLSGRVDMRQIEKTQYLIQSGMDPR	180			
Dd	154	VREDTGASPTPWAIWTRAWTAENRHGDLLHQYLVSGRVDMRQIOKTIQYLIQSGMDPR	213			
Qy	181	TENSPYLGFIYTSFOERATFTISHGNTARQAKEHGDIKLAQICGTAADEKRHETAYTKIV	240			
Dd	214	TENSPYLGFIYTSFOERATFISHGNTARHAKDYDGKLKAQICGTAADEKRHETAYTKIA	273			
Qy	241	EKLFEIDPDGTVLAFADMMWRKKISMPAHLMYVDGRDNLFDHESAVALRGVVTAKDYADI	300			
Dd	274	EKLFEIDPDGTVLAFADMMWRKKISMPAHLMYDGRDDLLFDHESAVALRGVVTAKDYADI	333			
Qy	301	LEFLVGRWKVKDLTGLSAGQKAQDYVCRLPPRIIRLEERAQGRAKEAPTMPFSWIFDRQ	360			
Dd	334	LEFLVGRWKVADLTGLSGEGRKAQDYVCGLPISRIRLEERAAAARAKEGPSIPFSWIFDRQ	393			
Qy	361	VKL 363				
Dd	394	VKL 396				
RESULT 7	O24498					
ID O24498	PRELIMINARY:	PRT.	396 AA.			



[illegible]

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QY 361 VKL 363
DB 394 VKL 396

RESULT 9
Q39355 PRELIMINARY; PRT; 401 AA.
ID Q39355 AC Q39355
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (stearoyl-ACP
DE desaturase).
GN BNA.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. JET NEUF.
RX MEDLINE=94286739; PubMed=8016261;
RA Slocumbe S.P., Piffanelli P., Fairbairn D., Bowra S., Hatzopoulos H.,
RA T'siantis M., Murphy D.J.;
RT "Temporal and tissue specific regulation of a Brassica napus stearoyl-
RT acyl carrier protein desaturase gene.";
RL Plant Physiol. 104:1167-1176(1994).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL; AF172782; CAA52786.1; -.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 401 AA; 45482 MW; 1CCFBL5626270401 CRC64;

Query Match 88.6%; Score 1698; DB 10; Length 401;
Best Local Similarity 86.7%; Pred. No. 7.5e-131;
Matches 312; Conservative 30; Mismatches 18; Indels 0; Gaps 0;

QY 4 LKSGSKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENLVLHVKPVEK 63
DB 42 LSSSTKEVESLKKPTTPPKREVHVQVTHSMPPQKIEIFKSLDNWAEENLVLHVKPVEK 101
QY 64 PQDFLPDPSADGDFEQVRELRAKEIPDDYFVVLVGMNITEALPTVOTMLNTLDGVRD 123
DB 102 PQDFLPDPSADGDFEQVRELRAKEIPDDYFVVLVGMNITEALPTVOTMLNTLDGVRD 161
QY 124 ETGASPTSWAIWTRAWTAENRHGDLNKNLYLSGRVDMRQIEKTIQYILGSGMDPR 183
DB 162 ETGASPTSWAIWTRAWTAENRHGDLNKNLYLSGRVDMRQIEKTIQYILGSGMDPR 221
QY 184 SPYLGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTAADEKRHETAYTKIV 243
DB 222 NPYLGIYTSFOERATFVSHGNTARQAKEHGDIKLAQICGTAADEKRHETAYTKIV 281
QY 244 FEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYVYAKDYADILEF 303

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DB 282 LEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYVYAKDYADILEF 341
QY 304 LVGRWKVDKLTGLSAGCOKAQDYVCLPRLPRLERAGRAKEAPMTFPIWLFDRQVKL 363
DB 342 LVGRWKIESLSGLSGEGNAQEYLCLTPRIKRLDERAARAKKGPFIWLDHREVQL 401

RESULT 10
Q9SW87 PRELIMINARY; PRT; 409 AA.
ID Q9SW87 AC Q9SW87
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (stearoyl-ACP
DE desaturase).
OS Arachis hypogaea (Peanut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae;
OC Arachis.
OX NCBI_TaxID=3818;
RN [1]
RP SEQUENCE FROM N.A.
RA Tate P.L., Kochert G., Abbott A.G.;
RT "The phylogenetic relationship of the cultivated peanut (Arachis
RT hypogaea L.) to its wild relative based upon comparisons of stearoyl-
RT ACP desaturase sequences.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL; AF172728; AAD48495.1; -.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 409 AA; 46810 MW; 7C80926BD8534A58 CRC64;

Query Match 88.5%; Score 1696.5; DB 10; Length 409;
Best Local Similarity 87.2%; Pred. No. 1e-130;
Matches 319; Conservative 24; Mismatches 20; Indels 3; Gaps 1;

QY 1 ASTLKSKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENLVLHVKPVEK 60
DB 44 ASTLTSKEVENLKKPTTPPKREVHVQVTHSMPPQKIEIFKSLGNAEENLVLHVKPVEK 103
QY 61 CWQPDQLPDPSADGDFEQVRELRAKEIPDDYFVVLVGMNITEALPTVOTMLNTLDG 120
DB 104 CWQPDQLPEPSEDFEQVRELRAKEIPDDYFVVLVGMNITEALPTVOTMLNTLDG 163
QY 121 VRDETASPTSWAIWTRAWTAENRHGDLNKNLYLSGRVDMRQIEKTIQYILGSGMDPR 180
DB 164 VRDETASPTSWAIWTRAWTAENRHGDLNKNLYLSGRVDMRQIEKTIQYILGSGMDPR 223
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTAADEKRHETAYTKIV 240
DB 224 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTAADEKRHETAYTKIV 283

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Qy 241 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADI 300  
 Db 284 EKLEIDPDGTVMAFADMMRKKIAMPALHMYDGRDNLDFENYSAVAQRIGVYTKADYADI 343  
 Qy 301 LEFLVGRWKVDKLGSLNEGOKAODYVCRLLP---RIRRLERAGRAKEAPTMPFWSIF 357  
 Db 344 LEFLVARKVADLTGLSGEGRKAODYVCRCPRIIRRLERAGRAKESPRLKFSWIY 403  
 Qy 358 DROVKL 363  
 Db 404 DREVQL 409

RESULT 11  
 Q9XOR7  
 ID Q9XOR7 PRELIMINARY; PRT; 401 AA.  
 AC Q9XOR7;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).  
 DE FAB2.  
 GN Brassica juncea (Leaf mustard) (Indian mustard).  
 OS Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PUSA JAIKISAN;  
 RA Vageshbabu H.S., Kirti P.B., Chopra V.L.;  
 RT "Nucleotide sequence of the coding region of the plastidic delta-9-stearoyl-acyl-acyl carrier protein desaturase of Brassica juncea.";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.  
 CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).  
 CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
 DR EMBL; AF153420; AAD40245.1; -.  
 DR HSSP; P22337; 1AFR.  
 DR InterPro; IPR005067; FA\_desat.  
 DR InterPro; IPR001225; FA\_desaturase.  
 DR Pfam; PF03405; FA\_desaturase\_2; 1.  
 DR PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
 DR Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; Transit peptide.  
 KW Transit peptide.  
 SQ SEQUENCE 401 AA; 45504 MW; 1726DA429DCDF00EB CRC64;

Query Match 88.5%; Score 1695; DB 8; Length 401;  
 Best Local Similarity 86.4%; Pred. No. 1.3e-130;  
 Matches 311; Conservative 30; Mismatches 19; Indels 0; Gaps 0;

Qy 4 LKSGSKEVENLKKPMPREHVHVQVTHSMPPQKIEIFKSLDNWAEENLVHLKPVKQW 63  
 Db 42 LSSSTKEVESLKKPPTPPKREHVHVQVTHSMPPQKIEIFKSLDNWAEENLVHLKPVKQW 101  
 Qy 64 PQDFLPDPASGDFGQVRELRAKEIPDDYFVVLVGDMTTEALPTYQTMINTLDGVRD 123  
 Db 102 PQDFLPDPASGDFGQVRELRAKEIPDDYFVVLVGDMTTEALPTYQTMINTLDGVRD 161  
 Qy 124 ETGASPTSWAIWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYLGSGMDPRPTEN 183  
 ||||| ||:|||||

Db 162 ETGASPTSWAVTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYLGSGMDPRPTEN 221  
 Qy 184 SPYLGFIYTSQERATFTSHGNTARQAKEHGDILKLAQICGTAADEKREHETAYTKIVEKL 243  
 Db 222 NPYLGFYITSQERATFVSHGNTARQAKEHGDILKLAQICGTAADEKREHETAYTKIVEKL 281  
 Qy 244 FEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADILEF 303  
 Db 282 LEIDPDGTVVAFADMMRKKISMPAHLMYDGRDNLDFNFSVAQRLGVYTKADYADILEF 341  
 Qy 304 LVGRWKVDKLTGLSABGOKAODYVCRLLPPIRRLERAGRAKEAPTMPFWSIFDQVKL 363  
 Db 342 LAGRWKIESLSGLSGEGRKAQYELCGLTPIRRLERAGRAKKGPKIPFWSIHDREVQL 401

## RESULT 12

O65040  
 ID O65040 PRELIMINARY; PRT; 396 AA.  
 AC O65040;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).  
 DE FAD1.  
 GN Macfadyena unguis-cati.  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Bignoniaceae; Macfadyena.  
 OX NCBI\_TaxID=73871;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cahoon E.B., Shah S., Shanklin J., Browse J.;  
 RT "A Determinant of Substrate Specificity Predicted from the Acyl-ACP Desaturase of Developing Doxantha Seed.";  
 RL Plant Physiol. 0:0-0(1998).  
 CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.  
 CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).  
 CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
 DR EMBL; AF051134; AAC05293.1; -.  
 DR HSSP; P22337; 1AFR.  
 DR InterPro; IPR005067; FA\_desat.  
 DR InterPro; IPR001225; FA\_desaturase.  
 DR Pfam; PF03405; FA\_desaturase\_2; 1.  
 DR PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
 DR Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; Transit peptide.  
 KW Transit peptide.  
 SQ SEQUENCE 396 AA; 45231 MW; 0101A758556D5C57 CRC64; 1

Query Match 88.1%; Score 1688; DB 10; Length 396;  
 Best Local Similarity 87.3%; Pred. No. 4.8e-130;  
 Matches 317; Conservative 24; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ASTLKSKEVENLKKPMPREHVHVQVTHSMPPQKIEIFKSLDNWAEENLVHLKPVK 60  
 Db 34 AATLKSGLRDVETKKTSPAREHVHVQVTHSMPPQKIEIFKAMEDWAEENLVHLKPNVK 93  
 Qy 61 CWPQDFLPDPASGDFGQVRELRAKEIPDDYFVVLVGDMTTEALPTYQTMINTLDG 120  
 Db 94 CPQPDFLPDPASGDFGQVRELRAKEIPDDYFVVLVGDMTTEALPTYQTMINTWDG 153  
 Qy 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYLGSGMDPR 180  
 ||||| ||:|||||

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Db 154 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDGKLAQICGTIAADEKRHETATYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARLARDHGDFKLAQICGTIASDEKRHETATYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNDLDFHFSVAQRLGVYTAADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRRKKSMPDHFMYDGRDNDLDFHFSVAQRLGVYTAADYADI 333
Qy 301 LEFLVGRWKVKDLTGLSAGQKADQYVCRLLPRIRLEERAQGRAKEAPTMPSWIFDRQ 360
Db 334 LEHLVGRWKVKDLTGLSAGQKADQYVCGLPPIRIRLEERAQIRAKQAPRLPFSWIDRE 393
Qy 361 VKL 363
Db 394 VQL 396

RESULT 13
Q8VXJ7 PRELIMINARY; PRT; 396 AA.
AC Q8VXJ7;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Stearoyl-ACP desaturase I (EC 1.14.99.6).
GN SDI.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAS-8;
RT Martinez-Force E., Fernandez-Moya V., Garces R.;
RL "Stearoyl-ACP desaturases in high-stearic sunflower mutants.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242632; CAC80360.1; -
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; UNKNOWN_1.
KW Oxidoreductase.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAS-8;
RT Martinez-Force E., Fernandez-Moya V., Garces R.;
RL "Stearoyl-ACP desaturases in high-stearic sunflower mutants.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242632; CAC80360.1; -
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; UNKNOWN_1.
KW Oxidoreductase.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE 396 AA; 45087 MW; F439BA366C4EB211 CRC64;
Query Match 87.3%; Score 1673; DB 10; Length 396;
Best Local Similarity 87.1%; Pred. No. 8.2e-129;
Matches 316; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPMPREVHVQVTHSMPPQKIEFKSLDNWAEENLVLHKPVEK 60
Db 34 ASTIGSATTKVESTKKPFTPPREVHQVLSHMPQKIEFKSMGWAEDNLVLHKPVEK 93
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTYQTMLNTLDG 120
Db 94 CWAQDFLPDPASDGFMEQVELRAKEIPDDYFVVLVGMITEEALPTYQTMLNTLDG 153
Qy 121 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 180
Db 154 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDGKLAQICGTIAADEKRHETATYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARHAKHGDGKLAQMGCGIIAADEKRHETATYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNDLDFHFSVAQRLGVYTAADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNDLDFHFSVAQRLGVYTAADYADI 333
Qy 301 LEFLVGRWKVKDLTGLSAGQKADQYVCRLLPRIRIRLEERAQGRAKEAPTMPSWIFDRQ 360
Db 334 LEFLVGRWKVKDLTGLSAGQKADQYVCGLPPIRIRIRLEERAQGRAKEAPTMPSWIFDRQ 393
Qy 361 VKL 363
Db 394 VQL 396

RESULT 15
Q42591 PRELIMINARY; PRT; 407 AA.
ID Q42591
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Db 334 LEFLVGRWKVKDLTGLSAGQKADQYVCGLPPIRIRIRLEERNSARAKERNVVPFSWLDRE 393
Qy 361 VKL 363
Db 394 VQL 396

RESULT 14
Q8VXJ8 PRELIMINARY; PRT; 396 AA.
AC Q8VXJ8;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Stearoyl-ACP desaturase I (EC 1.14.99.6).
GN SDI.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAS-4;
RT Martinez-Force E., Fernandez-Moya V., Garces R.;
RL "Stearoyl-ACP desaturases in high-stearic sunflower mutants.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242631; CAC80359.1; -
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; UNKNOWN_1.
KW Oxidoreductase.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE 396 AA; 45062 MW; 2E4C366839EBB347 CRC64;
Query Match 87.2%; Score 1670; DB 10; Length 396;
Best Local Similarity 87.1%; Pred. No. 1.4e-128;
Matches 316; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPMPREVHVQVTHSMPPQKIEFKSLDNWAEENLVLHKPVEK 60
Db 34 ASTIGSATTKVESTKKPFTPPREVHQVLSHMPQKIEFKSMGWAEDNLVLHKPVEK 93
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTYQTMLNTLDG 120
Db 94 CWAQDFLPDPASDGFMEQVELRAKEIPDDYFVVLVGMITEEALPTYQTMLNTLDG 153
Qy 121 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 180
Db 154 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDGKLAQICGTIAADEKRHETATYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARHAKHGDGKLAQMGCGIIAADEKRHETATYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNDLDFHFSVAQRLGVYTAADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNDLDFHFSVAQRLGVYTAADYADI 333
Qy 301 LEFLVGRWKVKDLTGLSAGQKADQYVCRLLPRIRIRLEERAQGRAKEAPTMPSWIFDRQ 360
Db 334 LEFLVGRWKVKDLTGLSAGQKADQYVCGLPPIRIRIRLEERNSARAKERNVVPFSWXLNRE 393
Qy 361 VKL 363
Db 394 VQL 396

RESULT 15
Q42591 PRELIMINARY; PRT; 407 AA.
ID Q42591
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Search completed: March 7, 2003, 03:09:56  
Job time : 35 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:04:12 ; Search time 13 Seconds  
(without alignments)  
1158.147 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKSGSKEVENLKRPFMP.....RAKEAPMPFWIFDRQVKL 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1916	100.0	396	1	STAD_RICCO
2	1764	92.1	396	1	STAD_CUCSA
3	1752	91.4	396	1	STAD_CORTN
4	1738	90.7	411	1	STAD_SQYBN
5	1724.5	90.0	399	1	STAD_SPTOL
6	1698	88.6	398	1	STAD_BRANA
7	1680	87.7	399	1	STAS_BRANA
8	1662.5	86.8	393	1	STAD_ELAGV
9	1655	86.4	396	1	STAD_HELAN
10	1652	86.2	393	1	STAD_SOLCO
11	1649	86.1	390	1	STAD_OLLEU
12	1626	84.9	393	1	STAD_SOLTU
13	1610.5	84.1	397	1	STAD_GOSHI
14	1607	83.9	398	1	STAD_SIMCH
15	1583	82.6	390	1	STAD_ORYSA
16	1465	76.5	396	1	STAD_LINUS
17	1317	68.7	385	1	STAD_CORSA
18	104.5	5.5	665	1	TKT_BUCAI
19	101.5	5.3	3421	1	TEGU_HSVB
20	101	5.3	1188	1	S3B1_SCHPO
21	99.5	5.2	375	1	RIR2_ECOLI
22	98.5	5.1	1304	1	S3B1_HUMAN
23	98.5	5.1	1304	1	S3B1_MOUSE
24	98.5	5.1	1307	1	S3B1_XENLA
25	97.5	5.1	449	1	YBB9_SCHPO
26	97	5.1	820	1	SYL_CHLPN
27	97	5.1	2096	1	BP28_DROME
28	96.5	5.0	709	1	PNP_PHOLU
29	96	5.0	858	1	ALR2_YEAST
30	95.5	5.0	375	1	RIR2_SALTY
31	93.5	4.9	643	1	NOS3_ALCEU
32	93.5	4.9	671	1	VINE_HUMAN
33	92.5	4.8	578	1	YBX6_SCHPO

#### RESULT 1

ID	STAD_RICCO	STANDARD;	PRT;	396 AA.
AC	P22337;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Acyl-[acyl-carrier protein] desaturase, chloroplast precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase) (Delta(9) stearoyl-acyl carrier protein desaturase).			
DE	Ricinus communis (Castor bean).			
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid1; Malpighiales; Euphorbiales; Ricinus.			
OC	NCBI_TaxID=3988;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91172837; PubMed=2006187;			
RA	Shanklin J., Somerville C.R.;			
RT	"Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally unrelated to the animal and fungal homologs.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Endosperm;			
RA	Knutzon D.S., Scherer D.E., Schreckengost W.E.;			
RT	"Nucleotide sequence of a complementary DNA clone encoding stearoyl-acyl carrier protein desaturase from castor bean, Ricinus communis.";			
RL	Plant Physiol. 96:344-345(1991).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).			
RX	MEDLINE=97015109; PubMed=8861937;			
RA	Lindqvist Y., Huang W., Schneider G., Shanklin J.;			
RT	"Crystal structure of delta9 stearoyl-acyl carrier protein desaturase from castor seed and its relationship to other di-iron proteins.";			
RL	EMBO J. 15:4081-4092(1996).			
CC	-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACRYL CHAIN.			
CC	-!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2) = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.			
CC	-!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.			
CC	-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.			
CC	-!- SUBUNIT: HOMODIMER.			
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES.			
CC	-!- TISSUE SPECIFICITY: HIGHER LEVELS IN DEVELOPING SEEDS THAN IN LEAF AND ROOT TISSUES.			
CC	-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way			

Q04322 saccharomyc  
Q43848 solanum tub  
Q12955 homo sapien  
Q9wlm8 drosophila  
Q9ka72 bacillus na  
Q03585 thermoplasm  
Q10592 mycobacteri  
Q57775 methanococc  
P13267 bacillus su  
P56142 helicobacte  
P45825 mycobacteri  
P08032 mus musculu

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CC -----  
CC DBL; M59857; AAA74692.1; ALT\_INIT.  
DR EMBL; X56508; CAA39859.1; -  
DR PIR; S16463; OHCSAD.  
DR PIR; A39170; A39170.  
DR PDB; IAFR; 15-WAY-97.  
DR InterPro; IPR005067; FA\_desat.  
DR InterPro; IPR001225; FA\_desaturase.  
DR Pfam; PF03405; FA\_desaturase.2; 1.  
DR PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;  
KW Transit peptide; 3D-structure.  
FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).  
FT CHAIN 34 396 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.  
SQ SEQUENCE 396 AA; 45371 MW; E50D4725996392AF CRC64;

Query Match 100.0%; Score 1916; DB 1; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2e-140;  
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVEK 60  
DB 34 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVEK 93  
QY 61 CWQPDFLPDPSADGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 120  
DB 94 CWQPDFLPDPSADGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 153  
QY 121 VRDETASPTSWAIWTRAWTAENRHGDLNKKYLILSGRVDMRQIEKTIQYLLIGSGMDPR 180  
DB 154 VRDETASPTSWAIWTRAWTAENRHGDLNKKYLILSGRVDMRQIEKTIQYLLIGSGMDPR 213  
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDKLQAOICGTIAADKRKHETATYKIV 240  
DB 214 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDKLQAOICGTIAADKRKHETATYKIV 273  
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 300  
DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 333  
QY 301 LEFLVGRWKVDKLTGLTSAEGQKADQYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 360  
DB 334 LEFLVGRWKVDKLTGLTSAEGQKADQYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 393  
QY 361 VKL 363  
DB 394 VKL 396

RESULT 2  
STAD\_CUCSA STANDARD; PRT; 396 AA.  
ID STAD\_CUCSA AC P32061;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor  
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).  
OS Cucumis sativus (Cucumber).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
OX NCBI\_TaxID=3659;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Seedling cotyledon.  
RA Shanklin J., Mullins C., Somerville C.R.;  
RT "Sequence of a complementary DNA from Cucumis sativus L. encoding the  
RL stearoyl-acyl-carrier protein desaturase."  
PL Plant Physiol. 97:467-468(1991).

RN SEQUENCE FROM N.A.  
RX MEDLINE=91172837; PubMed=2006187;  
RA Shanklin J., Somerville C.;  
RT "Stearoyl-acyl-carrier-protein desaturase from higher plants is  
structurally unrelated to the animal and fungal homologs."  
RL Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).  
CC !- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A  
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL  
CC CHAIN.  
CC !- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)  
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.  
CC !- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.  
CC !- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY  
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE  
CC OILS.  
CC !- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC !- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF  
CC NONPHOTOSYNTHETIC TISSUES.  
CC !- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; M59858; AAA33130.1; -  
PIR; B39170; B39170.  
DR HSSP; P22337; IAFR.  
DR InterPro; IPR005067; FA\_desat.  
DR InterPro; IPR001225; FA\_desaturase.  
DR Pfam; PF03405; FA\_desaturase.2; 1.  
DR PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;  
KW Transit peptide.  
FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).  
FT CHAIN 34 396 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.  
FT CONFLICT 114 114 R -> V (IN REF. 2).  
FT CONFLICT 290 290 E -> D (IN REF. 2).  
SQ SEQUENCE 396 AA; 45583 MW; 2E19E894C106D4C8 CRC64;

Query Match 92.1%; Score 1764; DB 1; Length 396;  
Best Local Similarity 90.4%; Pred. No. 1e-128;  
Matches 328; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVEK 60  
DB 34 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVEK 93  
QY 61 CWQPDFLPDPSADGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 120  
DB 94 CWQPDFLPDPSADGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 153  
QY 121 VRDETASPTSWAIWTRAWTAENRHGDLNKKYLILSGRVDMRQIEKTIQYLLIGSGMDPR 180  
DB 154 VRDETASPTSWAIWTRAWTAENRHGDLNKKYLILSGRVDMRQIEKTIQYLLIGSGMDPR 213  
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDKLQAOICGTIAADKRKHETATYKIV 240  
DB 214 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDKLQAOICGTIAADKRKHETATYKIV 273  
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 300  
DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 333  
QY 301 LEFLVGRWKVDKLTGLTSAEGQKADQYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 360  
DB 334 LEFLVGRWKVDKLTGLTSAEGQKADQYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 393  
QY 361 VKL 363



Query Match	91.4%	Score 1752;	DB 1;	Length 396;
Best Local Similarity	90.1%	Pred. No. 8.6e-128;		
Matches 327;	Conservative	18;	Mismatches 18;	Indels 0;
				Gaps 0;

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KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 28 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 29 411 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 411 AA; 47282 MW; 2727C3BDC8C97BA8 CRC64;

Query Match 90.7%; Score 1738; DB 1; Length 411;
Best Local Similarity 89.4%; Pred. No. 1.1e-126;
Matches 322; Conservative 25; Mismatches 13; Indels 0; Gaps 0;

QY 1 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVK 60
DB 29 ASTLRSGSKEVENLKPFMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVK 88
QY 61 CWPQDFLPDPSGDFEQVRELRAKEIPDDYFVVLVGDMLTEALPTYOTMLNTLDG 120
DB 89 CWPQDFLPDPSGDFEQVRELRAKEIPDDYFVVLVGDMLTEALPTYOTMLNTLDG 148
QY 121 VRDETGAFTSWAINTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
DB 149 VRDETGAFTSWAINTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 208
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETATKIV 240
DB 209 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETATKIV 268
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHESAVAGRLGVYAKDYADI 300
DB 269 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHESAVAGRLGVYAKDYADI 328
QY 301 LEFLVGRWKVKDLTGLSAEGQKAQDYVCRPLPRIRLEERAQRAKEAPTMPFSWIFDR 360
DB 329 LEFLVGRWKVKDLTGLSAEGQKAQDYVCRPLPRIRLEERAQRAKEAPTMPFSWIFDR 388

RESULT 5
- STAD_SP10L STANDARD; PRT; 399 AA.
AC P28645;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bifolia; TISSUE=Cotyledon;
RX MEDLINE=92329733; PubMed=1627785;
RA Beppu T., Nishida I., Matsuo T., Murata N.;
RT "Nucleotide sequence of a cDNA clone encoding a precursor to
RT stearyl-(acyl-carrier-protein) desaturase from spinach, Spinacia
RT oleracea."
RL Plant Mol. Biol. 19:711-713(1992).
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES.
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC EMBL; X62898; CAA44687.1; -
CC PIR; S22480; OHSPAD.
CC HSSP; P22337; 1A9P.
CC InterPro; IPR005067; FA_desat.
CC InterPro; IPR001225; FA_desaturase.
CC Pfam; PF03405; FA_desaturase_2; 1.
CC PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 35 CHLOROPLAST.
FT CHAIN 36 399 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 399 AA; 45663 MW; 59B56E0609EA7CCC CRC64;

Query Match 90.0%; Score 1724.5; DB 1; Length 399;
Best Local Similarity 87.9%; Pred. No. 1.1e-125;
Matches 320; Conservative 27; Mismatches 16; Indels 1; Gaps 1;

QY 1 ASTLKSGS-KEVENLKPFMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVK 59
DB 36 ASTLRSGSKEVENLKPFMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVK 95
QY 60 KCWQDFLPDPSGDFEQVRELRAKEIPDDYFVVLVGDMLTEALPTYOTMLNTLD 119
DB 96 KCWQDFLPDPSGDFEQVRELRAKEIPDDYFVVLVGDMLTEALPTYOTMLNTLD 155
QY 120 GVRDETGAFTSWAINTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDP 179
DB 156 GAKDETGAFTSWAINTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDP 215
QY 180 RTENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETATKIV 239
DB 216 RTENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETATKIV 275
QY 240 VEKLFETDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHESAVAGRLGVYAKDYAD 299
DB 276 VEKLFETDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHESAVAGRLGVYAKDYAD 335
QY 300 LEFLVGRWKVKDLTGLSAEGQKAQDYVCRPLPRIRLEERAQRAKEAPTMPFSWIFDR 359
DB 336 LEFLVGRWKVKDLTGLSAEGQKAQDYVCRPLPRIRLEERAQRAKEAPTMPFSWIFDR 395
QY 360 QVKL 363
DB 396 QVKL 399

RESULT 6
- STAD_BRANA STANDARD; PRT; 398 AA.
AC P29108;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. R500;
RX MEDLINE=92212881; PubMed=1557366;
RA Knutzon D.S., Thompson G.A., Radke S.E., Johnson W.B., Knauf V.C.,
RA Kridel J.C.;
```



104 LPPASDGFEDQVKELREARELPDDYFVVLVGMITEALTYOTMLNTLQVREDTGA 163  
 128 SPTSMAITRAWTAENRRHGDLLNKYLXLSGRVDMRQIEKTIQYLLIGSGMDPRTPENSPYL 187  
 164 SPTSAVWTRAWTAENRRHGDLLNKYLXLSGRVDMRQIEKTIQYLLIGSGMDPRTPENPNYL 223  
 188 GFITYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIVEKLFETD 247  
 224 GFITYTSFQERATFVSHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIVEKLFETD 283  
 248 PDGTVLAFADMMRKKTSMPAHLMYDGRDNLDFHFSVAQRGLGVYTAQDYADILEFLVGR 307  
 284 PDGTVAFADMMRKKTSMPAHLMYDGRDNLDFHFSVAQRGLGVYTAQDYADILEFLVGR 343  
 308 WKYDKLTGLSAEQKADQYVCRLLPRIRLEERAQRAKEAPTMPFSWIFDROVKL 363  
 344 WRISTLTGLSGEGNAQEVLCGLTPRIIRLDERAQAARAKKPKIPFSWIHREVQL 399

RESULT 8  
 STAD\_ELAV STANDARD; PRT; 393 AA.  
 ID STAD\_HELAV STANDARD; PRT; 396 AA.  
 AC Q24428;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor  
 DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).  
 OS Elaeis guineensis var. tenera (Oil palm).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Areaceae; Arecaceae;  
 OC Coccolae; Elaeidinae; Elaeis.  
 OX NCBI\_TaxID=51953;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mesocarp;  
 RA Shah F.H., Rashid O.;  
 RT "Nucleotide sequence of a cDNA clone encoding stearyl-acyl-carrier-  
 protein from Elaeis guineensis var tenera.";  
 RL (in) Plant Gene Register PGR96-110.  
 CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A  
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL  
 CC CHAIN.  
 CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)  
 CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.  
 CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.  
 CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY  
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE  
 CC OILS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF  
 CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
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 CC EMBL; U68756; ABA41041.1; ALT\_INIT.  
 DR HSP; P22337; IAFR.  
 DR InterPro; IPR005067; FA\_desat.  
 DR InterPro; IPR001225; FA\_desaturase.  
 DR Pfam; PF03405; FA\_Desaturase\_2; 1.  
 DR PROSITE; PS00574; FATTY ACID DESATUR\_2; 1.  
 DR Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;  
 KW Transit peptide.  
 FT TRANSIT 1 31 CHLOROPLAST (BY SIMILARITY).  
 FT CHAIN 32 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.

SQ SEQUENCE 393 AA; 44857 MW; C6A8788B80D9A0CC CRC64;  
 Query Match 86.8%; Score 1662.5; DB 1; Length 393;  
 Best Local Similarity 85.7%; Pred No. 6.7e-121;  
 Matches 311; Conservative 29; Mismatches 22; Indels 1; Gaps 1;  
 QY 1 ASTLSKSGSEVENLKKPPMPREHVHVQVTHSMPPQKIEIFKSLDNMAENILVHLKPVK 60  
 DB 32 ASTVGPSTK-VEIPKPPMPREHVHVQVTHSMPPQKIEIFKSLDNMAENILVHLKPVK 90  
 QY 61 CWQPDFLPDASDGFDEQVRELRAKEIPDDYFVVLVGMITEALTYOTMLNTLQV 120  
 DB 91 CWQPDFLPDSEGFHEEVKELEKRSKEIPDGYVCLVGMITEALTYOTMLNTLQV 150  
 QY 121 VDETCASPTSAIWTATRAWTAENRRHGDLLNKYLXLSGRVDMRQIEKTIQYLLIGSGMDPR 180  
 DB 151 VDETCASLTSWAVWTRAWTAENRRHGDLLNKYLXLSGRVDMRQIEKTIQYLLIGSGMDPR 210  
 QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIV 240  
 DB 211 TENSPLYGFIYTSFQERATFISHGNTARHAKHEGDIKLAQICGTIAADEKRHETAYTKIV 270  
 QY 241 EKLFEIDPDGTVLAFADMMRKKTSMPAHLMYDGRDNLDFHFSVAQRGLGVYTAQDYADI 300  
 DB 271 EKLFEIDPDGTVLFSFADMMRKKTSMPAHLMYDGRDNLDFHFSVAQRGLGVYTAQDYADI 330  
 QY 301 LEFLVGRMKVDKLTGLSAEQKADQYVCRLLPRIRLEERAQRAKEAPTMPFSWIFDRQ 360  
 DB 331 LEFLINRWKVGELTGLSGEGNAQDFVCTLAPRIIRLEERAQRAKEAPTMPFSWIVGRE 390  
 QY 361 VKL 363  
 DB 391 VQL 393  
 RESULT 9  
 STAD\_HELAV STANDARD; PRT; 396 AA.  
 ID STAD\_HELAV STANDARD; PRT; 396 AA.  
 AC Q96456;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor  
 DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).  
 OS Helianthus annuus (Common sunflower).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; easterids II; Asterales; Asteraceae; Asteroideae;  
 OC Heliantheae; Helianthus.  
 OX NCBI\_TaxID=4232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. SME3;  
 RA Coughlan S.J., Hastings C.E., Winfrey R.J.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A  
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL  
 CC CHAIN.  
 CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)  
 CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.  
 CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.  
 CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY  
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE  
 CC OILS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF  
 CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
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 CC -----  
 CC EMBL; U68756; ABA41041.1; ALT\_INIT.  
 DR HSP; P22337; IAFR.  
 DR InterPro; IPR005067; FA\_desat.  
 DR InterPro; IPR001225; FA\_desaturase.  
 DR Pfam; PF03405; FA\_Desaturase\_2; 1.  
 DR PROSITE; PS00574; FATTY ACID DESATUR\_2; 1.  
 DR Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;  
 KW Transit peptide.  
 FT TRANSIT 1 31 CHLOROPLAST (BY SIMILARITY).  
 FT CHAIN 32 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.

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CC -----
DR EMBL; U70374; AAB09571.1; -.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 34 396 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 396 AA; 45078 MW; 97E455A116791B81 CRC64;

Query Match 86.4%; Score 1655; DB 1; Length 396;
Best Local Similarity 86.5%; Pred. No. 2.6e-120;
Matches 314; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

Qy 1 ASTLKSQSGKEVENLKKPMPREHVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 34 ASTIGSATTKVESTKPTTPREHVHQVLSMPPQKIEIFKSMGWAENILVHLKPVEK 93

Qy 61 CWQPDFLPDPSADGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLGG 120
Db 94 CWQAQDFLPDPSADGFMQVEELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLGG 153

Qy 121 VRDETGAFTSWA IWTAWTAENRHGDLNKLKYLKSLGRVDMRQTEKTYQYIGSGMDPR 180
Db 154 VRDETGAFTLLGLVWTRAWTAENRHGDLNKLKYLKSLGRVDMRQTEKTYQYIGSGMDPR 213

Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKRHETATYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARHAKHEGDIKLAQICGTAADEKRHETATYTKIV 273

Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTAQDYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTAQDYADI 333

Qy 301 LEFLVGRWKVKDLTGLSAGQKADYVCLPRLPRIRLEERAQGRAKEAPTMPFSWIFDRQ 360
Db 334 LEFLVGRWKVADLTGLSGEGKADYVCGGLAPRIRLEERASARAKESVNVFWSWIFDRQ 393

Qy 361 VKL 363
Db 394 VKL 396

RESULT 10
STAD_SOLCO STANDARD; PRT; 393 AA.
ID STAD_SOLCO
AC Q41319;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Solanum commersonii (Commerson's wild potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4109;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Truccu M., Grillo S., Costa A., Leone A.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC C15 DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + A(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
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CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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EMBL; X78935; CA45535.1; -.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; FALSE_NEG.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 30 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 31 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 393 AA; 44765 MW; 5516E84FBF2C9501 CRC64;

Query Match 86.2%; Score 1652; DB 1; Length 393;
Best Local Similarity 84.8%; Pred. No. 4.3e-120;
Matches 308; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

Qy 1 ASTLKSQSGKEVENLKKPMPREHVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 31 ASTLPPSPVEDGNVKKPFPPREHVHVQVTHSMPPKEKREIFDSLHGWNADNNILHGLKPVEK 90

Qy 61 CWQPDFLPDPSADGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLGG 120
Db 91 CWQAQDFLPDPSADGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLGG 150

Qy 121 VRDETGAFTSWA IWTAWTAENRHGDLNKLKYLKSLGRVDMRQTEKTYQYIGSGMDPR 180
Db 151 VRDETGAFTSWA IWTAWTAENRHGDLNKLKYLKSLGRVDMRQTEKTYQYIGSGMDPR 210

Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKRHETATYTKIV 240
Db 211 TENNPFLGFIYTSFOERATFISHGNTARHAKHEGDMKLAQVCGIIAADKREHETATYTKIV 270

Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTAQDYADI 300
Db 271 EKLFEVDPDGTVLAVADMRRKKISMPAHLMYDGRDNLDFEHFSTVAQRLGVYTAQDYADI 330

Qy 301 LEFLVGRWKVKDLTGLSAGQKADYVCLPRLPRIRLEERAQGRAKEAPTMPFSWIFDRQ 360
Db 331 LEFLVGRWEIEKLTGLSGEGKADYVCGGLAPRIRKLEERAQAKQAPVPFSWVFGKD 390

Qy 361 VKL 363
Db 391 VKL 393

RESULT 11
STAD_OLEEU STANDARD; PRT; 390 AA.
ID STAD_OLEEU
AC Q43593;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Olea europaea (Common olive).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;


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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Oleaceae; Olea.  
 OX NCBI\_TaxID=4146;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Leccino; TISSUE=Mesocarp;  
 RA Baldoni L., Georgi L., Abbott A.G.;  
 RT "Nucleotide sequence of a cDNA clone from Olea europaea encoding a  
 RT stearyl-acyl carrier protein desaturase";  
 RL Plant Gene Register PGR96-052.  
 CC (-) FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A  
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL  
 CC CHAIN.  
 CC (-) CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)  
 CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.  
 CC (-) COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.  
 CC (-) PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY  
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE  
 CC OILS.  
 CC (-) SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC (-) SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF  
 CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).  
 CC (-) SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
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 CC -----  
 CC EMBL; U58141; AAB67840.1; -;  
 CC HSP; P22337; IAFR.  
 CC InterPro; IPR005067; FA\_desat.  
 CC InterPro; IPR001225; FA\_desaturase.  
 CC Pfam; PF03405; FA\_desaturase.2; 1.  
 CC PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
 CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;  
 CC Transit peptide.  
 CC TRANSIT 1 27 CHLOROPLAST (BY SIMILARITY).  
 CC CHAIN 28 390 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.  
 CC SEQUENCE 390 AA; 44596 MW; 39090EA32B7AC2E3 CRC64;  
 CC -----  
 CC Query Match 85.1%; Score 1649; DB 1; Length 390;  
 CC Best Local Similarity 85.1%; Pred. No. 7.3e-120;  
 CC Matches 309; Conservative 24; Mismatches 30; Indels 0; Gaps 0;  
 CC -----  
 CC QY 1 ASTLKSQSVENLKKPPPPREHVHVQVTHSMPPQKIEIFKSLDNWAEENLVHLKPVKE 60  
 CC DB 28 ASTHSPSMYGVKVKPPPPREHVHVQVTHSLAPEKREIFNLSNWAQENLVLLKDVDR 87  
 CC -----  
 CC QY 61 CWPQDFLPDPSGDFEQVRELRAKEIPDDYFVVLVGMITEEALPTQTMLNTLDG 120  
 CC DB 88 CWPQDFLPDPSGDFEQVRELRAKEIPDDYFVVLVGMITEEALPTQTMLNTLDG 147  
 CC -----  
 CC QY 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLVSGRVDMQIEKTIQYLVGMDPR 180  
 CC DB 148 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLVSGRVDMQIEKTIQYLVGMDPR 207  
 CC -----  
 CC QY 181 TENSPLYGLFYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRIHETAYTKIV 240  
 CC DB 208 TENSPLYGLFYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRIHETAYTKIV 267  
 CC -----  
 CC QY 241 EKLFEIDPDGTVLAFADMMRKISMPAHLMYDGRDNLDFHESAVALRGVYTTAKDYADI 300  
 CC DB 268 EKLFEIDPDGTVLAFADMMRKISMPAHLMYDGRDNLDFHESAVALRGVYTTAKDYADI 327  
 CC -----  
 CC QY 301 LEFLVGRWVWKLGLSREGQAQDYVCRPLPRIRRLERAAQGRKAKEAPTFWFSIFDRQ 360  
 CC DB 328 LEFLVGRWVWKLGLSREGQAQDYVCRPLPRIRRLERAAQGRKAKEAPTFWFSIFDRQ 387  
 CC -----  
 CC QY 361 VKL 363

DB 388 INL 390  
 RESULT 12  
 STAD\_SOLUTU STANDARD; PRT; 393 AA.  
 AC P46253;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor  
 DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Taylor M.A., Smith S.B., Davies H.V., Burch L.R.;  
 RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.  
 CC (-) FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A  
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL  
 CC CHAIN.  
 CC (-) CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)  
 CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.  
 CC (-) COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.  
 CC (-) PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY  
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE  
 CC OILS.  
 CC (-) SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC (-) SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF  
 CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).  
 CC (-) SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; M91238; AAA33839.1; -;  
 CC HSP; P22337; IAFR.  
 CC InterPro; IPR005067; FA\_desat.  
 CC InterPro; IPR001225; FA\_desaturase.  
 CC Pfam; PF03405; FA\_desaturase.2; 1.  
 CC PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
 CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;  
 CC Transit peptide.  
 CC TRANSIT 1 30 CHLOROPLAST (BY SIMILARITY).  
 CC CHAIN 31 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.  
 CC SEQUENCE 393 AA; 44538 MW; 3FBCC28D57CA7FF CRC64;  
 CC -----  
 CC Query Match 84.9%; Score 1626; DB 1; Length 393;  
 CC Best Local Similarity 82.4%; Pred. No. 4.4e-118;  
 CC Matches 299; Conservative 34; Mismatches 30; Indels 0; Gaps 0;  
 CC -----  
 CC QY 1 ASTLKSQSVENLKKPPPPREHVHVQVTHSMPPQKIEIFKSLDNWAEENLVHLKPVKE 60  
 CC DB 31 ASTHSPSMYGVKVKPPPPREHVHVQVTHSMPPQKIEIFKSLDNWAEENLVHLKPVKE 90  
 CC -----  
 CC QY 61 CWPQDFLPDPSGDFEQVRELRAKEIPDDYFVVLVGMITEEALPTQTMLNTLDG 120  
 CC DB 91 CWPQDFLPDPSGDFEQVRELRAKEIPDDYFVVLVGMITEEALPTQTMLNTLDG 150  
 CC -----  
 CC QY 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLVSGRVDMQIEKTIQYLVGMDPR 180  
 CC DB 151 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLVSGRVDMQIEKTIQYLVGMDPR 210  
 CC -----  
 CC QY 181 TENSPLYGLFYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRIHETAYTKIV 240

[illegible]

Db	215	ENSPYRGFIYTSQERATFISHGNTGRLAKKEYGDINLAQCGSASDEKRRHETAYTKIVE	274
QY	242	KLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVVYTKADYADIL	301
Db	275	KLFEIDPDQTVLAFADMMRKKIAMPAEFIVDGRDYNLFHDYSAVAQRLGVVYTKADYDIV	334
QY	302	EFLVGRWKKVDKLTGLSAGOKAQVYCRLLPPIRRLRERAAQGRK - EAPTMPPFSWIFDRQ	360
Db	335	EHLVDRWKKVELAGLSAEGRKAQDYLCSPRSIRRLRERAAQKAQGSTVSPFSWIFDRE	394
QY	361	VKL 363	
Db	395	VKL 397	

RESULT 14

STAD_SIMCH	STANDARD;	PRT;	398 AA.
ID	Q01753;		
AC	01-APR-1993 (Rel. 25, Created)		
DT	01-APR-1993 (Rel. 25, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	EC1-[acyl-carrier protein] desaturase, chloroplast precursor		
DE	(P. 14, 99-6) (Stearoyl-ACP desaturase).		
OS	Simmondsia chinensis (Jojoba).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Caryophyllales; Caryophyllaceae; Simmondsiaceae; Simmondsia.		
NCBI	TaxID=3999;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Sato A., Becker C.K., Knauf V.C.;		
RT	"Nucleotide sequence of a complementary DNA clone encoding stearoyl-		
RT	acyl carrier protein desaturase from Simmondsia chinensis.";		
RL	Plant Physiol. 99:362-363(1992).		
CC	-!- FUNCTION: STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A		
CC	CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL		
CC	CHAIN.		
CC	-!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)		
CC	= oleoyl-[acyl-carrier protein] + A + 2 H(2)O.		
CC	-!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.		
CC	-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY		
CC	ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE		
CC	OILS.		
CC	SUBUNIT: HOMODIMER.		
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF		
CC	-!- NONPHOTOSYNTHETIC TISSUES.		
CC	-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.		

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DR EMBL; M83199; AAA33932.1; -.
DR HSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 34 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 35 398 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 398 AA; 45130 MW; F3E000BB044427D8 CRC64;

Query Match 83.9%; Score 1607; DB 1; Length 398;
Best Local Similarity 81.8%; Pred. No. 1.3e-116;
Matches 297; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

QY 1 ASTLKSSEVENLKKPFPPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVEK 60
DB 36 SSTIGITSKEIPNAKKPHMPPREAHVQKTHSMPPQKIEIFKSLDGEWAENVLVHLKPVEK 95
QY 61 CWPQDFLPDPASGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTLG 120
DB 96 CWPQDFLPDPASGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTLG 155
QY 121 VRDETASPTSWAIWTRAMTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
DB 156 VRDETASPTSWAIWTRAMTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 215
QY 181 TENSPLYGFIYTSFQERATFISGNTARQAKHGDIKLAQICGTIAADEKRHETAYTKIV 240
DB 216 SENPYLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGTIAADEKRHETAYTKIV 275
QY 241 EKLFEIDPDGCTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 300
DB 276 EKLFEIDPDGCTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 335
QY 301 LEFLVGRWKVDKLTGSLAEGQKADYVCRPLPPRIRLEERAQRAKEAPTMPFSWIFDRQ 360
DB 336 LEFLVGRWKVDKLTGSLAEGQKADYVCRPLPPRIRLEERAQRAKEAPTMPFSWIFDRQ 395
QY 361 VKL 363
DB 396 LKV 398

RESULT 15
STAD_ORYSA STANDARD; PRT; 390 AA.
AC Q40731;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ACYL-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare; TISSUE=Seed;
RX MEDLINE=95334510; PubMed=7610181;
RA Akagi H., Baba T., Shimada H., Fujimura T.;
RT "Nucleotide sequence of a stearyl-acyl carrier protein desaturase
RT cDNA from developing seeds of rice.";
RL Plant Physiol. 108:845-846(1995).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.

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CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC
CC EMBL; D38753; BAA07631.1; -.
CC HSP; P22337; IAFR.
CC InterPro; IPR005067; FA_desat.
CC InterPro; IPR001225; FA_desaturase.
CC Pfam; PF03405; FA_desaturase_2; 1.
CC PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 31 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 32 390 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 390 AA; 44482 MW; ED974E4C1E285597 CRC64;

Query Match 82.6%; Score 1583; DB 1; Length 390;
Best Local Similarity 81.0%; Pred. No. 8.9e-115;
Matches 294; Conservative 35; Mismatches 30; Indels 4; Gaps 1;

QY 1 ASTLKSSEVENLKKPFPPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVEK 60
DB 32 ASTI---NRVKTAKPYTPPREVHLQVKHSLPPQKREIFDSLQPWAKENLLNLLKPVEK 87
QY 61 CWPQDFLPDPASGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTLG 120
DB 88 SWQPDFLPDPSSGDFYVEKELRAKEIPDDYFVCLVGDMMYTEALPTQYTMNLTLG 147
QY 121 VRDETASPTSWAIWTRAMTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
DB 148 VRDETASPTSWAIWTRAMTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPG 207
QY 181 TENSPLYGFIYTSFQERATFISGNTARQAKHGDIKLAQICGTIAADEKRHETAYTKIV 240
DB 208 TENNPYLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGTIAADEKRHETAYTKIV 267
QY 241 EKLFEIDPDGCTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 300
DB 268 EKLFEIDPDGCTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 327
QY 301 LEFLVGRWKVDKLTGSLAEGQKADYVCRPLPPRIRLEERAQRAKEAPTMPFSWIFDRQ 360
DB 328 LEFLVGRWKVDKLTGSLAEGQKADYVCRPLPPRIRLEERAQRAKEAPTMPFSWIFDRQ 387
QY 361 VKL 363
DB 388 VQL 390

```

Search completed: March 7, 2003, 03:09:10  
Job time: 15 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:07:27 ; Search time 22 Seconds  
(without alignments)  
1586.218 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKSQSGKEVENLKKPFMP.....RAKEAFTMPFSWIFDRQVKL 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1916	100.0	396	1 OHCSAD	acyl-[acyl-carrier
2	1760	91.9	396	2 B39170	acyl-[acyl-carrier
3	1752	91.4	396	1 A39173	acyl-[acyl-carrier
4	1738	90.7	411	2 T07806	acyl-[acyl-carrier
5	1733	90.4	401	2 E84869	stearoyl-ACP desat
6	1727	90.1	396	2 T14264	acyl-[acyl-carrier
7	1724.5	90.0	399	1 OHSPAD	acyl-[acyl-carrier
8	1701	88.8	396	2 T14268	acyl-[acyl-carrier
9	1698	88.6	398	2 S23351	acyl-[acyl-carrier
10	1680	87.7	399	2 S24995	acyl-[acyl-carrier
11	1660.5	86.7	407	2 S71264	acyl-[acyl-carrier
12	1655	86.4	396	2 T14172	acyl-[acyl-carrier
13	1652	86.2	393	2 S44202	acyl-[acyl-carrier
14	1626	84.9	393	2 T07653	acyl-[acyl-carrier
15	1610.5	84.1	397	2 T10793	acyl-[acyl-carrier
16	1583	82.6	390	2 T04097	acyl-[acyl-carrier
17	1526.5	79.7	394	2 T51494	stearoyl-acyl carr
18	1465	76.5	396	2 S31959	acyl-[acyl-carrier
19	1358	70.9	401	2 T51493	stearoyl-acyl carr
20	1318	68.8	374	2 A96502	probable acyl-acyl
21	1317	68.7	385	2 A47245	acyl-[acyl-carrier
22	307	16.0	328	2 T35035	probable acyl-facy
23	272	14.2	338	2 D70810	probable desA1 pro
24	267	13.9	338	2 D87182	acyl-[ACP] desatur
25	158	8.2	275	2 C87153	acyl-[ACP] desatur
26	138	7.2	275	2 D70896	probable desA2 pro
27	112.5	5.9	389	2 D82223	ribonucleoside-dip
28	112.5	5.9	1155	2 G87477	transcription-repa
29	108	5.6	744	2 T09541	transketolase (EC

30	105.5	5.5	558	2 A75216	hypothetical prote
31	105.5	5.5	1490	2 JC5145	DNA (cytosine-5)-
32	105	5.5	874	2 AC3070	ATP-dependent Clp
33	105	5.5	887	2 F98216	endopeptidase clp
34	104.5	5.5	665	2 E84940	transketolase (EC
35	102.5	5.3	1322	2 T24140	hypothetical prote
36	102	5.3	3643	2 T36410	probable polyketid
37	101.5	5.3	3421	1 WZBE66	367K tegument prot
38	101	5.3	1188	2 T38467	hypothetical nuclea
39	100	5.2	652	2 T20046	hypothetical prote
40	99.5	5.2	376	1 RDEC2R	ribonucleoside-dip
41	99.5	5.2	376	2 F91018	ribonucleoside-dip
42	99.5	5.2	376	2 H85862	ribonucleoside-dip
43	98.5	5.1	598	2 D95207	oligoendopeptidase
44	98.5	5.1	598	2 D98072	oligoendopeptidase
45	98.5	5.1	1307	2 T30887	146D nuclear prote

ALIGNMENTS

RESULT 1

OHCSAD

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - castor bean  
N:Alternate names: stearoyl-[acyl-carrier-protein] desaturase  
C:Species: Ricinus communis (castor bean)  
C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 03-Jun-2002

C:Accession: S16463; A39170

R:Knutzon, D.S.; Scherer, D.E.; Schreckengost, W.E.

Plant Physiol. 96, 344-345, 1991

A:Title: Nucleotide sequence of a complementary DNA clone encoding stearoyl-acyl carr

A:Reference number: S16463

A:Accession: S16463

A:Molecule type: mRNA

A:Residues: 1-396 <KNU>

A:Cross-references: EMBL:X56508; NID:g21092; PIDN:CAA39859.1; PID:g21093

R:Shanklin, J.; Somerville, C.

Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991

A:Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally

A:Reference number: A39170; MUID:91172837; PMID:2006187

A:Accession: A39170

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-396 <SHA>

A:Cross-references: GB:M59858

A:Note: parts of this sequence were confirmed by peptide sequencing

C:Superfamily: acyl-facyl-carrier-protein desaturase

C:Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase

F:1-33/Domain: transit peptide (chloroplast) #status predicted <TNP>

F:34-396/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match 100.0%; Score 1916; DB 1; Length 396;

Best Local Similarity 100.0%; Pred. No. 6.7e-137;

Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASTLKSQSGKEVENLKKPFMPREHVQVTHSMPPKQIEIFKSLDWAENILVHLKPVKE 60

Db 34 ASTLKSQSGKEVENLKKPFMPREHVQVTHSMPPKQIEIFKSLDWAENILVHLKPVKE 93

Oy 61 CWQPDQFLDPASDGFDEQVRELREAKEIPDDYFVVLVGDMMITEALPTYQTMNLTDG 120

Db 94 CWQPDQFLDPASDGFDEQVRELREAKEIPDDYFVVLVGDMMITEALPTYQTMNLTDG 153

Oy 121 VRDEGTASPTSWAIWTRAWTAENRHGDLNLLKYLVSGRVDMRQIEKTIQYUIGSGMDPR 180

Db 154 VRDEGTASPTSWAIWTRAWTAENRHGDLNLLKYLVSGRVDMRQIEKTIQYUIGSGMDPR 213

Oy 181 TENSPLYGFITTSFOERATFTSHGNTARQAKHGDIKLAQICGTIAADKRETHETATKIV 240

Db 214 TENSPLYGFITTSFOERATFTSHGNTARQAKHGDIKLAQICGTIAADKRETHETATKIV 273

Oy 241 EKLFEIDPDGTVLAFAFAMMRKKISMFAHLMYDGRDNLFDHFSAVAQRLGVVYATKDYADI 300

Db 241 EKLFEIDPDGTVLAFAFAMMRKKISMFAHLMYDGRDNLFDHFSAVAQRLGVVYATKDYADI 300

Db 274 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSVAQRLGVYTKADYADI 333  
Qy 301 LEFLVGRWKVKDTGLTGLSAGQKADQYVCRLLPRIRLEERAQRAKEAPTMPSWIFDRQ 360  
Db 334 LEFLVGRWKVKDTGLTGLSAGQKADQYVCRLLPRIRLEERAQRAKEAPTMPSWIFDRQ 393  
Qy 361 VKL 363  
Db 394 VKL 396

RESULT 2  
B39170  
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - cucumber  
C:Species: Cucumis sativus (cucumber)  
C>Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 03-Jun-2002  
C:Accession: B39170  
R:Shanklin, J.; Somerville, C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991  
A:Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally und  
A:Reference number: A39170; MUID:91172837; PMID:2006187  
A:Accession: B39170  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-396 <SHA>  
A:Cross-references: GB:M59857  
C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
C:Keywords: chloroplast; oxidoreductase

Query Match 91.9%; Score 1760; DB 2; Length 396;  
Best Local Similarity 90.4%; Pred. No. 3.9e-125;  
Matches 328; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNDNAEENILVHLKPVEK 60  
Db 34 ASTLRSTSEVELKKPFMPREVHVQVTHSMPPQKIEIFKSLDNDNAEENILVHLKPVEK 93  
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLG 120  
Db 94 CWPQDFLPDPAFEGFQVVELRAKELPDEVFVVLVGDMMITEALPTYQTMNLTLG 153  
Qy 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLIGSGMDPR 180  
Db 154 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLIGSGMDPR 213  
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTITADEKRRHETAYTKIV 240  
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTITADEKRRHETAYTKIV 273  
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSVAQRLGVYTKADYADI 300  
Db 274 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSVAQRLGVYTKADYADI 333  
Qy 301 LEFLVGRWKVKDTGLTGLSAGQKADQYVCRLLPRIRLEERAQRAKEAPTMPSWIFDRQ 360  
Db 334 LEFLVGRWKVKDTGLTGLSAGQKADQYVCRLLPRIRLEERAQRAKEAPTMPSWIFDRQ 393  
Qy 361 VKL 363  
Db 394 VKL 396

RESULT 3  
A39173  
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - safflower  
C:Species: Carthamus tinctorius (safflower)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
C:Accession: A39173  
R:Thompson, G.A.; Scherer, D.E.; Foxall-Van Aken, S.; Kenny, J.W.; Young, H.L.; Shintani  
Proc. Natl. Acad. Sci. U.S.A. 88, 2578-2582, 1991  
A:Title: Primary structures of the precursor and mature forms of stearoyl-acyl carrier p  
A:Reference number: A39173; MUID:91172850; PMID:2006194  
A:Accession: A39173

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-396 <THO>  
A:Cross-references: GB:M61109; NID:g167196; PIDN:AAA33021.1; PID:g167197  
C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
C:Keywords: chloroplast; oxidoreductase

Query Match 91.4%; Score 1752; DB 1; Length 396;  
Best Local Similarity 90.1%; Pred. No. 1.6e-124;  
Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNDNAEENILVHLKPVEK 60  
Db 34 ASTLGSTPKVDNAKPFQPPREVHVQVTHSMPPQKIEIFKSLDNDNAEENILVHLKPVEK 93  
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLG 120  
Db 94 CWPQDFLPDPASEGDFEQVRELRAKELPDDYFVVLVGDMMITEALPTYQTMNLTLG 153  
Qy 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLIGSGMDPR 180  
Db 154 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLIGSGMDPR 213  
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTITADEKRRHETAYTKIV 240  
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTITADEKRRHETAYTKIV 273  
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSVAQRLGVYTKADYADI 300  
Db 274 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSVAQRLGVYTKADYADI 333  
Qy 301 LEFLVGRWKVKDTGLTGLSAGQKADQYVCRLLPRIRLEERAQRAKEAPTMPSWIFDRQ 360  
Db 334 LEFLVGRWKVKDTGLTGLSAGQKADQYVCRLLPRIRLEERAQRAKEAPTMPSWIFDRQ 393  
Qy 361 VKL 363  
Db 394 VKL 396

RESULT 4  
T07806  
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - soybean  
N:Alternate names: stearoyl-acyl carrier protein desaturase  
C:Species: Glycine max (soybean)  
C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 03-Jun-2002  
C:Accession: T07806  
R:Chen, B.Y.; Jones, H.W.  
submitted to the EMBL Data Library, July 1994  
A:Reference number: Z16145  
A:Accession: T07806  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-411 <CHE>  
A:Cross-references: EMBL:L34346; NID:g508602; PIDN:AAA92462.1; PID:g508603  
C:Genetics:  
A:Gene: SACPD  
A:Genome: nuclear  
C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
C:Keywords: chloroplast; oxidoreductase  
F:1-29/Domain: transit peptide (chloroplast) #status predicted <TNP>

Query Match 90.7%; Score 1738; DB 2; Length 411;  
Best Local Similarity 89.4%; Pred. No. 1.9e-123;  
Matches 322; Conservative 25; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNDNAEENILVHLKPVEK 60  
Db 29 ASTLRSGSKEVENIKKPFMPREVHVQVTHSMPPQKIEIFQSLDNDNAEENILVHLKPVEK 88  
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLG 120  
Db 89 CWPQDFLPDPSSDGFEEQVRELRAKELPDDYFVVLVGDMMITEALPTYQTMNLTLG 148

Qy	121	VRDETGA	PSWAIW	TRAWTA	EBNRHGD	LLNKYL	YLSGRV	DMRQ	IEKTI	QY	YLIG	SGMD	PR	180	
Db	149	VRDETGA	SLTWSAI	WTRAWTA	EBNRHGD	LLNKYL	YLSGRV	DMKQ	IEKTI	QY	YLIG	SGMD	PR	208	
Qy	181	TENSPY	LGFY	TSFO	ERATF	ISHGNT	AROK	EHGDI	KL	LAQ	ICGT	TAAD	SKRHET	ATY	240
Db	209	TENSPY	LGFY	TSFO	ERATF	ISHGNT	ARLAK	EHGDI	KL	LAQ	ICGM	TASD	SKRHET	ATY	268
Qy	241	EKLFEI	DPDGT	VLAFAD	MMRKK	ITSM	PAHLMY	DGRD	DNLF	DHFS	AVAQR	LGVV	TAKDY	ADI	300
Db	269	EKLFE	SPDGT	VNAFAD	MMRKK	ITAMP	PAHLMY	DGRD	DNLF	DNYS	SSVAQR	LGVV	TAKDY	ADI	328
Qy	301	LEFLVGR	WKVK	DKIT	GLS	ASGQ	KAQD	VYVCR	LP	PRIR	LEERA	GRAKE	APM	PFS	360
Db	329	LEFLVGR	WKVEQ	LTL	SGSGR	KAQ	EYIC	GLP	PRIR	LEERA	QARV	KESSTL	AFSH	IDHRE	388

```

RESULT 5
E84869
C:stearyl-ACP desaturase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-feb-2003
C:Accession: E84869
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, I.;
euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
A:Reference number: AB4420; MUID:20083487; PMID:10617197
A:Accession: E84869
A>Status: preliminary

```

A;Residues: 1-401 <STO>  
A;Cross-references: GB:AE02093; NID:g2281099; PIDN:AAB64035.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: At2g43710  
A;Map position: 2  
C;Superfamily: acyl-[acyl-carrier-protein] desaturase

	Query Match	90.4%	Score 1733;	DB 2:	Length 401;
	Best Local Similarity	89.4%;	Pred. No.	4.3e-133;	
	Matches 32;	Conservative	Mismatches 16;	Indels 0;	Gaps 0;
Qy	4	LKSGSKEVNIUKKFMPPREVVHVQVTISMPPQKIIEFKSLDNWAENILVLHKLVPVEKCWQ	63		
Dz	4	LSSGPKVESLUKKFTTPREVHVQLSHMPPQKIIEFKSMENWAENILLIHLKDVKESWQ	101		
Qy	64	PDDELPLDPSADGFDEQVRELRLERAKEIPDDYFVVLVGDMITEEALPTYTMLNTLDGVRD	123		
Dz	102	PDDELPLDPSADGFDEQVRELRLERARELPDDYFVVLVGDMITEEALPTYTMLNTLDGVRD	161		

Qy	124	ETGASPTSWAIWTRAWTAENRRHGDLLNKLYLUSGRVDMRQTEKTTQYLLIGSGMDPRTEN	183
Db	162	ETGASPTSWAIWTRAWTAENRRHGDLLNKLYLUSGRVDMRQIEKTTQYLLIGSGMDPRTEN	221
Qy	184	SPYLGFYLTFSQERATFISHGNTARQAKEHGDIKLQACGTAADEKRHETATYTKLVEKL	243
Db	222	NPYLGFYLTFSQERATFISHGNTARQAKEHGDIKLQACGTAADEKRHETATYTKLVEKL	281
Qy	244	FEIDPDGTVLAFADMMRRKKSIMPAHLMYDGRDNDLDFHSVAQRULGVVTKADYADILEF	303
Db	282	FEIDPDGTVMAFADMMRRKKSIMPAHLMYDGRDNDLDFNSSVAQRULGVVTKADYADILEF	341
Qy	304	LVGRWKVDKLTGLSABGQKAQDYVCRLLPPIRLERAPRAQRAKEAPMPFSWTFDQWKL	363
Db	342	LVGRWKIQDTLTGLSGEGNKAQDYLCGLAPRIKRLDERAPARAKKPKIFSWIHDFREVOL	401

RESULT 6  
T14264  
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower  
N:Alternate names: stearyl-ACP desaturase

C:Species: *Helianthus annuus* (common sunflower)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
C:Accession: T14264  
R:Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J.  
submitted to the EMBL Data Library, February 1997  
A:Description: Sunflower stearyl-ACP desaturase.  
A:Reference number: Z17946  
A:Accession: T14264  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-396 <HON>  
A:Cross-references: EMBL:U91339; NID:g2290399; PID:g2290400  
A:Experimental source: Strain Mammoth  
C:Function:  
C:Description: Introduces a double bond at the delta(9) position of stearoyl-ACP.  
C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
C:Keywords: fatty acid biosynthesis; oxidoreductase

[illegible]

## RESULT 7

QHPAD

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor

C:Species: Spinacia oleracea (spinach)

C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 03-Jun-2002

C;Accession: S22480; S18183

R;Nishida, I.; Beppu, T.; Matsuo, T.; Murata, N.

Plant Mol. Biol. 19, 711-713, 1992

A;Title: Nucleotide sequence of a  
X:Protein number: 522490: MULT: 9

A: Reference number: S  
A: Accession: S22480

A:ACCESSION: 322480  
A:MOLECULE TYPE: mRNA

A; Residues: 1-399 &lt;NI.

A;Cross-references: EMBL:X62898; NID:g21229; PIDN:CAA44687.1; PID:g21230

C;Superfamily: acyl-[acyl-carrier-protein] desaturase

**C;Keywords:** chloroplast; fatty acid biosynthesis; oxidoreductase

```
F;1-35/Domain: transit peptide (chloroplast) #status predicted <TNP>
```

F:36-399/Product: acyl-[acyl-carrier-protein] desaturase #status predicted &lt;MAI&gt;

Query Match

Query Match  
Best Local Similarity 87.98: Pred. No. 1.9e-122:  
50.0%, SCORE 1724.5, DB 1, Bengali 555

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Matches 320; Conservative 27; Mismatches 16; Indels 1; Gaps 1;

QY 1 ASTLKSGS-KEVENLKKPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVE 59  
 DB 36 ASTLSSSPKAEBSLKKPSPREVHVQVTHSMPPQKIEIFKSLGWAENILVHLKPVE 95  
 QY 60 KCWQPDLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTD 119  
 DB 96 KCWQPDLPDPASEDFRQVKEIQERAKEIPDDLYVLVGDMMITEALPTQYTMNLTD 155  
 QY 120 GVRDETGAFTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDP 179  
 DB 156 GADKETGASPTSWAVWTRAWTAENRHGDLNKKLYLSGRVDMRSTIEKTIQYILGSGMDP 215  
 QY 180 RTENSPYLGFIYTSFOERATFISHGNTARQAKEHGDILKLAQICGTIAADEKRHETAYTKI 239  
 DB 216 RTENSPYLGFIYTSFOERATFISHGNTARQAKEHGDILKLAQICGTIAADEKRHETAYTKI 275  
 QY 240 VEKLFEDPDGTVLAFADMMRKIKISPAHLMYDGRDNLDFHFSAVAQRLGVVYTKADYAD 299  
 DB 276 VEKLFEDPDGTVLAFADMMRKIKISPAHLMYDGRDNLDFHFSAVAQRLGVVYTKADYAD 335  
 QY 300 ILFELVGRWKVYDLTGLSABGQAQDYVCLPRIRRLERAQRAKEAPTMFPSWIFDR 359  
 DB 336 ILFELVGRWEVEKLTGLSSEGQAQDYVCSLPRIRRLERAQRAKEAPTMFPSWIFDR 395  
 QY 360 QVKL 363  
 DB 396 QVKL 399

RESULT 8  
 T14268  
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower  
 N:Alternate names: stearoyl-ACP desaturase  
 C:Species: Helianthus annuus (common sunflower)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
 C:Accession: T14268  
 R:Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J.  
 submitted to the EMBL Data Library, February 1997  
 A:Description: Sunflower stearoyl-ACP desaturase.  
 A:Reference number: Z17946  
 A:Accession: T14268  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-396 <HON>  
 A:CROSS-references: EMBL:U91340; NID:g2290401; PID:g2290402  
 A:Experimental source: strain Mammoth  
 C:Function:  
 A:Description: Introduces a double bond at the delta(9) position of stearoyl-ACP generated  
 A:Pathway: fatty acid biosynthesis  
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
 C:Keywords: fatty acid biosynthesis; oxidoreductase

Query Match 88.8%; Score 1701; DB 2; Length 396;  
 Best Local Similarity 88.4%; Pred. No. 1.1e-120;  
 Matches 321; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

QY 1 ASTLKSGKEVENLKKPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60  
 DB 34 ASTIGSATTKVEKPPPTPPREVHVQVTHSMPPQKIEIFKSLGWAENILVHLKPVEK 93  
 QY 61 CWQPDLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTD 120  
 DB 94 CWQPDLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTD 153  
 QY 121 VRDETGAFTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPR 180  
 DB 154 VRDETGAFTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPR 213  
 QY 181 TENSPLYLGFYTSFOERATFISHGNTARQAKEHGDILKLAQICGTIAADEKRHETAYTKIV 240  
 DB 214 TENSPLYLGFYTSFOERATFISHGNTARQAKEHGDILKLAQICGTIAADEKRHETAYTKIV 273

QY 241 EKLFEIDPDGTVLAFADMMRKIKISPAHLMYDGRDNLDFHFSAVAQRLGVVYTKADYADI 300  
 DB 274 EKLFEIDPDGTVLAFADMMRKIKISPAHLMYDGRDNLDFHFSAVAQRLGVVYTKADYADI 333  
 QY 301 LDFLVGRWKVYDLTGLSABGQAQDYVCLPRIRRLERAQRAKEAPTMFPSWIFDRQ 360  
 DB 334 LDFLVGRWKVYDLTGLSABGQAQDYVCLPRIRRLERAQRAKEAPTMFPSWIFDRQ 393  
 QY 361 VKL 363  
 DB 394 VKL 396

RESULT 9  
 S23351  
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - turnip  
 C:Species: brassica rapa (turnip)  
 C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-Jun-2002  
 C:Accession: S23351  
 R:Knutzon, D.S.; Thompson, G.A.; Radke, S.E.; Johnson, W.B.; Kridl, J.C.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2624-2628, 1992  
 A:Title: Modification of Brassica seed oil by antisense expression of a stearoyl-acyl  
 A:Reference number: S23351; MUID:92212881; PMID:1557366  
 A:Accession: S23351  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-398 <KNU>  
 A:CROSS-references: EMBL:X60978; NID:g17928; PID:CAA43294.1; PID:g17929  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991  
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
 C:Keywords: chloroplast; oxidoreductase

Query Match 88.6%; Score 1698; DB 2; Length 398;  
 Best Local Similarity 88.2%; Pred. No. 1.9e-120;  
 Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 8 SKEVENLKKPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKQWQDF 67  
 DB 43 SKEVESLKKPPTPPKEVHVQVTHSMPPQKIEIFKSLGWAENILVHLKPVEKQWQDF 102  
 QY 68 LPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTDGVRDETGA 127  
 DB 103 LPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTDGVRDETGA 162  
 QY 128 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTPNSPYL 187  
 DB 163 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTPNNPYL 222  
 QY 188 GFITYTSFOERATFISHGNTARQAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLEID 247  
 DB 223 GFITYTSFOERATFISHGNTARQAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLEID 282  
 QY 248 PDGTVLAFADMMRKIKISPAHLMYDGRDNLDFHFSAVAQRLGVVYTKADYADILEFLVGR 307  
 DB 283 PDGTVLAFADMMRKIKISPAHLMYDGRDNLDFHFSAVAQRLGVVYTKADYADILEFLVGR 342  
 QY 308 WKYDKLTGLSABGQAQDYVCLPRIRRLERAQRAKEAPTMFPSWIFDRQVKL 363  
 DB 343 WKIESLTGLSGEKNKAQYELCGLTPRIRRLERAQRAKKGPKVPFWSWIHDREVOL 398

RESULT 10  
 S24995  
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - rape  
 N:Alternate names: stearoyl-[acyl-carrier-protein] desaturase  
 C:Species: Brassica napus (rape)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 03-Jun-2002  
 C:Accession: S24995  
 R:Slocumbe, S.P.; Cummins, I.; Jarvis, R.P.; Murphy, D.J.  
 Plant Mol. Biol. 20, 151-155, 1992  
 A:Title: Nucleotide sequence and temporal regulation of a seed-specific Brassica napu  
 A:Reference number: S24995; MUID:92385757; PMID:1515603

A:Accession: S24995  
A:Molecule type: mRNA  
A:Residues: 1-399 <SFO>  
A:Cross-references: EMBL:X63364; NID:gl7869; PIDN:CAA44964.1; PID:gl7870  
C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
C:Keywords: chloroplast; fatty acid biosynthesis; homodimer; oxidoreductase

Query Match 87.7%; Score 1680; DB 2: Length 399;  
Best Local Similarity 87.1%; Pred. No. 4.2e-119; Mismatches 17; Indels 0; Gaps 0;  
Matches 310; Conservative 29;

Qy 8 SKEVENLKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVKQWQDF 67  
Db 44 SKEVESLKPPTPPREVHLQVLSMPPQKIEIFKSMEDRAEQNLPLHLKDVESQWQDF 103

Qy 68 LPDPASDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDGVRDETGA 127  
Db 104 LPDPASDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDGVRDETGA 163

Qy 128 SPTSWAIWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYILGSGMDPRTENSPLY 187  
Db 164 SPTSWAVWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYILGSGMDPRTENNPYL 223

Qy 188 GFIVTSFOERATFISHGNTARQAHEGDIKLAQICGTIAADEKRHETAYTKIVEKLEFID 247  
Db 224 GFIVTSFOERATFVSHGNTARQAHEGDLKLAQICGTIAADEKRHETAYTKIVEKLEID 283

Qy 248 PDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTAADYADILEFLVGR 307  
Db 284 PDGTVAFADMMRKKISMPAHLMYDGRDNLFDNFSSVAQRLGVYTAADYADILEFLAGR 343

Qy 308 WKVDKLTGLSAGOKAQDYVCRLLPRIRRLERAQRAKEAPTMPFSEIFDQVKL 363  
Db 344 WRIESLGLSGEGNAQDYELCLTPRIRRLDERAQAARKGPKIPFSEIHDREVQL 399

RESULT 11

\* S71264  
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - Arabidopsis thaliana  
N:Alternate names: Stearoyl-ACP desaturase  
C:Species: Arabidopsis thaliana. (mouse-ear cress)  
C:Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 03-Jun-2002  
C:Accession: S71264  
R:Piffanelli, P.; Murphy, D.J.  
submitted to the EMBL Data Library, November 1995  
A:Description: Cloning of a stearoyl-ACP desaturase from Arabidopsis thaliana.  
A:Reference number: S71264  
A:Accession: S71264  
A:Molecule type: mRNA  
A:Residues: 1-407 <PIF>  
A:Cross-references: EMBL:X93461; NID:gl107506; PIDN:CAA63746.1; PID:gl107507  
C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
C:Keywords: fatty acid biosynthesis; oxidoreductase

Query Match 86.7%; Score 1660.5; DB 2: Length 407;  
Best Local Similarity 87.9%; Pred. No. 1.3e-117; Mismatches 21; Conservative 21;

Qy 4 LKSSKEVENLKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVKQWQ 63  
Db 42 LSSGKEVESLKPPTPPREVHVQVLSMPPQKIEIFKSMENWAEENILHLKDVESQW 101

Qy 64 QDPLPDPSDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDGVRD 123  
Db 102 QDPLPDPSDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDGVRD 161

Qy 124 ETGASPTSWAIWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYILGSGMDPRTEN 183  
Db 162 ETGASPTSWAIWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYILGSGMDPRTEN 221

Qy 184 SPYLGFIYTSFOERATFISHGNTARQAHEGDIKLAQICGTIAADEKRHETAYTKIVEKL 243  
Db 222 NPYLGFIYTSFOERATFISHGNTARQAHEGDIKLAQICGTIAADEKRHETAYTKIVEKL 281

Qy 244 FEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTAADYADILEF 303  
Db 282 FEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDNFSSVAQRLGVYTAADYADILEF 341

Qy 304 LVGRWKVDKLTGLSAGOKAQDYVCRLLPRIRRLERAQRAKEAPTMP 352  
Db 342 LVGRWKIQDLTGLSGEGNAQDYLCGLAPRIKRLDERAQAARKLGQKQKPLP 395

RESULT 12

T14172  
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower  
N:Alternate names: Stearoyl-ACP desaturase  
C:Species: Helianthus annuus (common sunflower)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
C:Accession: T14172  
R:Coughlan, S.J.; Hastings, C.E.; Winfrey, R.J.  
submitted to the EMBL Data Library, September 1996  
A:Description: Sunflower stearoyl-ACP desaturase.  
A:Reference number: Z17901  
A:Accession: T14172  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-396 <COU>  
A:Cross-references: EMBL:U70374; NID:gl575696; PID:gl575697  
A:Experimental source: strain SMF3  
C:Function:  
A:Description: introduces a double bond at the delta(9) position of stearoyl-ACP gene  
A:Pathway: fatty acid biosynthesis  
C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
C:Keywords: fatty acid biosynthesis; oxidoreductase

Query Match 86.4%; Score 1655; DB 2: Length 396;  
Best Local Similarity 86.5%; Pred. No. 3.2e-117; Mismatches 19; Conservative 31; Indels 0; Gaps 0;

Qy 1 ASTLKSKEVENLKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVK 60  
Db 34 ASTIGSATTKVESTKPKPTPPREVHQVLSMPPQKIEIFKSMENWAEENILVHLKPVK 93

Qy 61 CWQOPDFLPDPASDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDG 120  
Db 94 CWQAQDFLPDPASDGFMEQVEELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDG 153

Qy 121 VRDETGAFTSWAIWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYILGSGMDP 180  
Db 154 VRDETGAFTLLGLVWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYILGSGMDP 213

Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAHEGDIKLAQICGTIAADEKRHETAYTKIV 240  
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAHEGDIKLAQICGTIAADEKRHETAYTKIV 273

Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTAADYADI 300  
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDNFSSVAQRLGVYTAADYADI 333

Qy 301 LEFLVGRWKVDKLTGLSAGOKAQDYVCRLLPRIRRLERAQRAKEAPTMPFSEIFDQ 360  
Db 334 LEFLVGRWKVADLTGLSGEGNAQDYVCGCLAPRIKRLDERAQAARKLGQKQKPLP 393

Qy 361 VKL 363  
Db 394 VKL 396

RESULT 13

S44202  
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - Commerson's wild po  
N:Alternate names: Stearoyl-ACP desaturase  
C:Species: Solanum commersonii (Commerson's wild potato)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 03-Jun-2002  
C:Accession: S44202

R:Trucci, M.; Grillo, S.; Costa, A.; Leone, A.  
 Submitted to the EMBL Data Library, April 1994  
 A:Reference number: S44202  
 A:Accession: S44202  
 A:Molecule type: mRNA  
 A:Residues: 1-393 <TRU>  
 A:Cross-references: EMBL:X78935; NID:g474832; PIDN:CAA55535.1; PID:g474833  
 C:Genetics:

A:Genome: nuclear  
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
 C:Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase  
 F:1-30/Domain: transit peptide (chloroplast) #status predicted <NP>  
 F:31-393/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match 86.2%; Score 1652; DB 2; Length 393;  
 Best Local Similarity 84.8%; Pred. No. 5.4e-117;  
 Matches 308; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

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QY 1 ASTLKSGSKEVENLKPFMPREHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVEK 60
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31 ASTLRPSVEDGNVKKPFPREHVQVTHSMPPKEKEVDFSLRDWAAQNLLVHLKPVEK 90
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CWOQDFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMINTLDG 120
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 CWOQDFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMINTLDG 150
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 VRDETGAAPTWSAIWTRAWTAENRHGDLNKLKYLILSGRVDMDROIETIQYLIGSGMDPR 180
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 VRDETGATVTPWAIWTRAWTAENRHGDLNKLKYLILSGRVDMDROIETIQYLIGSGMDPR 210
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 240
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 TENNPHLGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 270
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 EKLEIPDGTGLAFADMRKKNISPAHLMYDGRDNLDFHFSVAQORGLGVYTKADYADI 300
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 EKLEVPDGTGLAFADMRKKNISPAHLMYDGRDNLDFHFSVAQORGLGVYTKADYADI 330
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 LEFLVGRWKVDKLTGLSAEGOKAQDYVCRLLPRIRLEERAQGRAKEAPTMPSWIFDRQ 360
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 LEFLVGRWEIEKLTGLSGEGHAKRDYVCGGLAPRIKLEERAQARAKAPVPFSWIFGKD 390
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 VKL 363
   |||
Db 391 IKL 393
   |||

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## RESULT 14

T07653  
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - potato  
 N:Alternate names: stearoyl-acyl carrier protein desaturase  
 C:Species: Solanum tuberosum (potato)  
 C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 03-Jun-2002  
 C:Accession: T07653  
 R:Taylor, M.A.; Smith, S.B.; Davies, H.V.; Burch, L.R.  
 submitted to the EMBL Data Library, April 1992  
 A:Description: The primary structure of a cDNA clone of the stearoyl-acyl carrier protein  
 A:Reference number: Z16073  
 A:Accession: T07653  
 A:Molecule type: mRNA  
 A:Residues: 1-393 <TAY>  
 A:Cross-references: EMBL:M91238; NID:g169564; PIDN:AAA33839.1; PID:g169565  
 C:Genetics:  
 A:Genome: nuclear  
 C:Function:  
 A:Description: catalyzes the formation of double bonds at the delta(9) position of stera  
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
 C:Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase

Query Match 84.9%; Score 1626; DB 2; Length 393;  
 Best Local Similarity 82.4%; Pred. No. 4.9e-115;  
 Matches 299; Conservative 34; Mismatches 30; Indels 0; Gaps 0;

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QY 1 ASTLKSGSKEVENLKPFMPREHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVEK 60
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31 ASTLRPSVEDGNVKKPFPREHVQVTHSMPPKEKEVDFSLRDWAAQNLLVHLKPVEK 90
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CWOQDFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMINTLDG 120
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 CWOQDFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMINTLDG 150
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 VRDETGAAPTWSAIWTRAWTAENRHGDLNKLKYLILSGRVDMDROIETIQYLIGSGMDPR 180
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 VRDETGATVTPWAIWTRAWTAENRHGDLNKLKYLILSGRVDMDROIETIQYLIGSGMDPR 210
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 240
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 TENNPHLGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 270
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 EKLEIPDGTGLAFADMRKKNISPAHLMYDGRDNLDFHFSVAQORGLGVYTKADYADI 300
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 EKLEVPDGTGLAFADMRKKNISPAHLMYDGRDNLDFHFSVAQORGLGVYTKADYADI 330
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 LEFLVGRWKVDKLTGLSAEGOKAQDYVCRLLPRIRLEERAQGRAKEAPTMPSWIFDRQ 360
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 LEFLVGRWEIEKLTGLSGEGHAKRDYVCGGLAPRIKLEERAQARAKAPVPFSWIFGKE 390
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 VKL 363
   |||
Db 391 IKL 393
   |||

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RESULT 15  
 T10793  
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - upland cotton  
 N:Alternate names: delta 9 stearoyl-acyl-carrier protein desaturase  
 C:Species: Gossypium hirsutum (upland cotton)  
 C:Date: 18-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 03-Jun-2002  
 C:Accession: T10793  
 R:Liu, Q.; Singh, S.; Sharp, P.; Green, A.; Marshall, D.R.  
 Plant Physiol. 110, 1436, 1996  
 A:Title: Nucleotide sequence of a cDNA from Gossypium hirsutum encoding a stearoyl-ac  
 A:Reference number: Z17148  
 A:Accession: T10793  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-397 <LIU>  
 A:Cross-references: EMBL:X95988; NID:g1217627  
 A:Experimental source: cultivar deltapine-16  
 C:Function:  
 A:Description: Introduces a double bond at the delta(9) position of stearoyl-ACP gene  
 A:Pathway: fatty acid biosynthesis  
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase  
 C:Keywords: fatty acid biosynthesis; oxidoreductase; unsaturated fatty acid biosynthe  
 F:1-65/Domain: signal sequence #status predicted <SIG>  
 F:66-397/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match 84.1%; Score 1610.5; DB 2; Length 397;  
 Best Local Similarity 84.0%; Pred. No. 7.3e-114;  
 Matches 305; Conservative 21; Mismatches 36; Indels 1; Gaps 1;

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QY 2 STLKSGSKEVENLKPFMPREHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVEK 61
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 35 STIPSGSKEVENLKPFMPREHVQVTHSMPPKHIEFKSLGWAENNLTLHLKPVEK 94
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 WOPQDFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMINTLDG 121
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 95 WOPADFLPDNSGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMINTLDG 154
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 122 RDETGAAPTWSAIWTRAWTAENRHGDLNKLKYLILSGRVDMDROIETIQYLIGSGMDPR 181
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 155 RDETGAAPTWSAIWTRAWTAENRHGDLNKLKYLILSGRVDMDROIETIQYLIGSGMDPR 214
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 182 ENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIVE 241
   |||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 215 ENSPYRGEIYTSFOERATFISHGNTGRLAKEYGDIINLAQICGSIASDEKRHETAYTKIVE 274  
Qy 242 KLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDDNLFDFHSAVAQRLGVYTKADYADIL 301  
Db 275 KLFEIDPDGTVLAFADMMRKKIAMPAAEFYDGRDYNLFDFHSAVAQRLGVYTKADYVDIV 334  
Qy 302 EFLVGRWKVKLTGLSABGQKAQDYVCRLPPIRRLRLEERAQGRK-EAPTMPFSWIFDRQ 360  
Db 335 EHLVDRWKVKELAGLSABGRKAQDYLCSLPSRIRRLRLEERAQEGKAQGSTPVSPFSWIFDRE 394  
Qy 361 VKL 363  
Db 395 VKL 397

Search completed: March 7, 2003, 03:10:30  
Job time : 23 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2003, 03:10:02 ; Search time 16 Seconds  
(without alignments)  
956.736 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKSGSKEVENLKPKFMP.....RAKEAPTMPSWIFDROVKL 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1916	100.0	363	10	US-09-988-929A-1
2	1916	100.0	363	12	US-10-017-145-1
3	1637	85.4	396	10	US-09-837-751-2
4	291	15.2	54	9	US-09-730-763-12
5	291	15.2	54	9	US-09-730-763-16
6	286	14.9	54	9	US-09-730-763-13
7	283	14.8	54	9	US-09-730-763-15
8	276	14.4	54	9	US-09-730-763-18
9	273	14.2	52	9	US-09-730-763-27
10	271	14.1	52	9	US-09-730-763-31
11	270	14.1	54	9	US-09-730-763-17
12	270	14.1	54	9	US-09-730-763-14
13	267	13.9	338	9	US-09-730-763-4
14	267	13.9	338	9	US-09-730-763-37
15	262	13.7	52	9	US-09-730-763-28
16	260	13.6	52	9	US-09-730-763-29
17	255	13.3	54	9	US-09-730-763-19
18	254	13.3	52	9	US-09-730-763-33
19	247	12.9	52	9	US-09-730-763-30

20	232	12.1	52	9	US-09-730-763-32	Sequence 32, Appl
21	213	11.1	52	9	US-09-730-763-34	Sequence 34, Appl
22	102.5	5.3	54	9	US-09-730-763-20	Sequence 20, Appl
23	97.5	5.1	1049	10	US-09-815-242-10732	Sequence 10732, A
24	96	5.0	858	8	US-08-945-749-2	Sequence 2, Appl
25	94.5	4.9	447	10	US-09-815-242-13412	Sequence 13412, A
26	94.5	4.9	447	10	US-09-815-242-13590	Sequence 13590, A
27	90.5	4.7	1189	10	US-09-815-242-10552	Sequence 10552, A
28	87.5	4.6	393	9	US-09-895-913A-172	Sequence 172, App
29	87.5	4.6	393	10	US-09-881-752A-152	Sequence 152, App
30	87	4.5	368	9	US-09-738-626-4393	Sequence 4393, Ap
31	87	4.5	451	9	US-10-028-072-126	Sequence 126, App
32	87	4.5	451	9	US-10-121-049-126	Sequence 126, App
33	87	4.5	451	9	US-10-123-904-126	Sequence 126, App
34	87	4.5	451	9	US-10-140-470-126	Sequence 126, App
35	87	4.5	451	9	US-10-175-746-126	Sequence 126, App
36	87	4.5	451	9	US-10-176-918-126	Sequence 126, App
37	87	4.5	451	9	US-10-176-921-126	Sequence 126, App
38	87	4.5	451	9	US-10-137-865-126	Sequence 126, App
39	87	4.5	451	9	US-10-140-474-126	Sequence 126, App
40	87	4.5	451	9	US-10-142-431-126	Sequence 126, App
41	87	4.5	451	9	US-10-143-114-126	Sequence 126, App
42	87	4.5	451	9	US-10-140-002-126	Sequence 126, App
43	87	4.5	1169	10	US-09-815-242-13448	Sequence 13448, A
44	87	4.5	1169	10	US-09-815-242-13693	Sequence 13693, A
45	87	4.5	1460	10	US-09-815-242-13668	Sequence 13668, A

#### ALIGNMENTS

RESULT 1

US-09-988-929A-1

; Sequence 1, Application US/09988929A

; Patent No. US20020150982A1

; GENERAL INFORMATION:

; APPLICANT: Brookhaven Science Associates

; APPLICANT: Shanklin, John

; APPLICANT: Cahoon, Edgar B

; TITLE OF INVENTION: Mutant Fatty Acid Desaturase

; FILE REFERENCE: BSA 02-01; CIP of 09/233,856, filed 01/19/99

; CURRENT APPLICATION NUMBER: US/09/988,929A

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 09/233,856

; PRIOR FILING DATE: 1999-01-19

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1

; LENGTH: 363

; TYPE: PRT

; ORGANISM: Ricinus communis

US-09-988-929A-1

Query Match 100.0%; Score 1916; DB 10; Length 363;  
Best Local Similarity 100.0%; Pred. No. 7.8e-169;  
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKPKFMPPREVHVQVTHSMPPKIEIFKSLDNWAEENILVHLKPVK 60

Db 1 ASTLKSGSKEVENLKPKFMPPREVHVQVTHSMPPKIEIFKSLDNWAEENILVHLKPVK 60

Qy 61 CWQPDFLPDASDGFDEQVRELREKIPDDYFVVLVGDMTTEALPTYQTMINTL 120

Db 61 CWQPDFLPDASDGFDEQVRELREKIPDDYFVVLVGDMTTEALPTYQTMINTL 120

Qy 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLKSLGRVDMRQIEKTIQYLLIGSGMDPR 180

Db 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLKSLGRVDMRQIEKTIQYLLIGSGMDPR 180

Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTAADEKRHETAYTKIV 240

Db 181 TENSPLYGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTAADEKRHETAYTKIV 240

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QY 241 EKLEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNLFDHFSVAQRLGVYTKDYADI 300
Db 241 EKLEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNLFDHFSVAQRLGVYTKDYADI 300
QY 301 LEFLVGRWKVDKLTGLSAGQKADYVCRPLPRIRLRLEERAQRAKEAPTPFWSIFDRQ 360
Db 301 LEFLVGRWKVDKLTGLSAGQKADYVCRPLPRIRLRLEERAQRAKEAPTPFWSIFDRQ 360
QY 361 VKL 363
Db 361 VKL 363

RESULT 2
US-10-017-145-1
; Sequence 1, Application US/10017145
; Patent No. US20020151019A1
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates
; TITLE OF INVENTION: Mutant Fatty Acid Desaturase and Methods for Directed Mutagenesis
; FILE REFERENCE: CIP of 09/328,550 filed June 9, 1999; which was a CIP of 09/233,856
; January 19, 1999
; CURRENT APPLICATION NUMBER: US/10/017,145
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 09/328,550
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Ricinus communis
; NAME/KEY: misc_feature
; OTHER INFORMATION: ricinus communis delta 9 18:0 Acyl ACP Desaturase
US-10-017-145-1

Query Match 100.0%; Score 1916; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 7 8e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTLKSKEVENLKKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 1 ASTLKSKEVENLKKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
QY 61 CWPQDELDPDPSDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTVOTMLNTLDG 120
Db 61 CWPQDELDPDPSDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTVOTMLNTLDG 120
QY 121 VRDETGAAPTSAIWTAWTAENRHGDLNKLKYLKYLGRVDMRQIEKTIQYLLIGSGMDPR 180
Db 121 VRDETGAAPTSAIWTAWTAENRHGDLNKLKYLKYLGRVDMRQIEKTIQYLLIGSGMDPR 180
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTTAADEKREHETAYTKIV 240
Db 181 TENSPLYGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTTAADEKREHETAYTKIV 240
QY 241 EKLEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNLFDHFSVAQRLGVYTKDYADI 300
Db 241 EKLEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNLFDHFSVAQRLGVYTKDYADI 300
QY 301 LEFLVGRWKVDKLTGLSAGQKADYVCRPLPRIRLRLEERAQRAKEAPTPFWSIFDRQ 360
Db 301 LEFLVGRWKVDKLTGLSAGQKADYVCRPLPRIRLRLEERAQRAKEAPTPFWSIFDRQ 360
QY 361 VKL 363
Db 361 VKL 363

RESULT 3
US-09-837-751-2
; Sequence 2, Application US/09837751
; Patent No. US20020104124A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Liu, Qing
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
; FILE REFERENCE: 45-00
; CURRENT APPLICATION NUMBER: US/09/837,751
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,124
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Gossypium sp.
US-09-837-751-2

Query Match 85.4%; Score 1637; DB 10; Length 396;
Best Local Similarity 85.1%; Pred. No. 4 8e-143;
Matches 308; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 2 STLKSGSKEVENLKKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 61
Db 35 STIPSGSKEVENLKKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 94
QY 62 WQPDDELDPDPSDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTVOTMLNTLDG 121
Db 95 WQPDDELDPDPSDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTVOTMLNTLDG 154
QY 122 RDETGAAPTSAIWTAWTAENRHGDLNKLKYLKYLGRVDMRQIEKTIQYLLIGSGMDPR 181
Db 155 RDETGAAPTSAIWTAWTAENRHGDLNKLKYLKYLGRVDMRQIEKTIQYLLIGSGMDPR 214
QY 182 TENSPLYGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTTAADEKREHETAYTKIVE 241
Db 215 TENSPLYGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTTAADEKREHETAYTKIVE 274
QY 242 KLFEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNLFDHFSVAQRLGVYTKDYADI 301
Db 275 KLFEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDNLFDHFSVAQRLGVYTKDYADI 334
QY 302 EFLVGRWKVDKLTGLSAGQKADYVCRPLPRIRLRLEERAQRAKEAPTPFWSIFDRQ 361
Db 335 EFLVGRWKVDKLTGLSAGQKADYVCRPLPRIRLRLEERAQRAKEAPTPFWSIFDRQ 394
QY 362 KL 363
Db 395 KL 396

RESULT 4
US-09-730-763-12
; Sequence 12, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIQUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahbow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/730,763  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/917,299  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0156-00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-730-763-12

Query Match 15.2%; Score 291; DB 9; Length 54;  
Best Local Similarity 100.0%; Pred. No. 3.7e-20;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 98 LVGDMITEALPTYQTMINTLDGVRDETGA SPTS WAIWTRAWTAENRHGDLN 151  
|||||  
Db 1 LVGDMITEALPTYQTMINTLDGVRDETGA SPTS WAIWTRAWTAENRHGDLN 54

RESULT 5  
US-09-730-763-16  
Sequence 16, Application US/09730763  
Publication No. US20020192781A1  
GENERAL INFORMATION:  
APPLICANT: JACKSON, Mary  
APPLICANT: GIQUEL, Brigitte  
TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O Finnegan Henderson, Farrahaw, Garrett &  
ADDRESSEE: Dunner, L.L.P  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/730,763  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/917,299  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0156-00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:  
LENGTH: 54 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-730-763-16

Query Match 15.2%; Score 291; DB 9; Length 54;  
Best Local Similarity 100.0%; Pred. No. 3.7e-20;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 98 LVGDMITEALPTYQTMINTLDGVRDETGA SPTS WAIWTRAWTAENRHGDLN 151  
|||||  
Db 1 LVGDMITEALPTYQTMINTLDGVRDETGA SPTS WAIWTRAWTAENRHGDLN 54

RESULT 6  
US-09-730-763-13  
Sequence 13, Application US/09730763  
Publication No. US20020192781A1  
GENERAL INFORMATION:  
APPLICANT: JACKSON, Mary  
APPLICANT: GIQUEL, Brigitte  
TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O Finnegan Henderson, Farrahaw, Garrett &  
ADDRESSEE: Dunner, L.L.P  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/730,763  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/917,299  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0156-00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-730-763-13

Query Match 14.9%; Score 286; DB 9; Length 54;  
Best Local Similarity 98.1%; Pred. No. 1.1e-19;  
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 98 LVGDMITEALPTYQTMINTLDGVRDETGA SPTS WAIWTRAWTAENRHGDLN 151  
|||||  
Db 1 LVGDMITEALPTYQTMINTLDGVRDETGA SPTS WAIWTRAWTAENRHGDLN 54

RESULT 7

2

; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 52 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-730-763-27

Query Match 14.2%; Score 273; DB 9; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.6e-18;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 186 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRKHETAYT 237  
|||||  
Db 1 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRKHETAYT 52

## RESULT 10

US-09-730-763-31  
; Sequence 31, Application US/09730763  
; Publication No. US20020192781A1  
; GENERAL INFORMATION:

; APPLICANT: JACKSON, Mary  
; APPLICANT: GIQUEL, Brigitte  
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Finnegan Henderson, Farrabow, Garrett &  
; ADDRESSEE: Dunner, L.L.P.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09730,763  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/917,299  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:  
; NAME: MEYERS, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03495.0156-00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 52 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-730-763-31

Query Match 14.1%; Score 271; DB 9; Length 52;  
Best Local Similarity 98.1%; Pred. No. 2.5e-18;  
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 186 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRKHETAYT 237  
|||||  
Db 1 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRKHETAYT 52

## RESULT 11

US-09-730-763-17  
; Sequence 17, Application US/09730763  
; Publication No. US20020192781A1  
; GENERAL INFORMATION:

; APPLICANT: JACKSON, Mary  
; APPLICANT: GIQUEL, Brigitte  
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Finnegan Henderson, Farrabow, Garrett &  
; ADDRESSEE: Dunner, L.L.P.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09730,763  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/917,299  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:  
; NAME: MEYERS, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03495.0156-00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 54 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-730-763-17

Query Match 14.1%; Score 271; DB 9; Length 54;  
Best Local Similarity 90.7%; Pred. No. 2.6e-18;  
Matches 49; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 98 LVGDMITEALPTYOTMLNTLDGVRDETGCASPTSWAIVTRAHTAENRHGDLN 151  
|:|||||  
Db 1 LIGDMITEALPTYOTMLNTLDGVRDETGCATVTPWAIVTRAHTAENRHGDLN 54

## RESULT 12

US-09-730-763-14  
; Sequence 14, Application US/09730763  
; Publication No. US20020192781A1  
; GENERAL INFORMATION:

; APPLICANT: JACKSON, Mary  
; APPLICANT: GIQUEL, Brigitte  
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Finnegan Henderson, Farrabow, Garrett &  
; ADDRESSEE: Dunner, L.L.P.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-730-763-14

Query Match      14.1%; Score 270; DB 9; Length 54;
Best Local Similarity 92.6%; Pred. No. 3.2e-18;
Matches 50; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 98 LVGDMITEEALPTVQTMINTLDGVYRDETASPTSWAIWTRAWTAENRHGDLIN 151
Db 1 LVGDMITEEALPTVQTMINTLDGVYRDETASPTSWAIWTRAWTAENRHGDLIN 54

RESULT 13
US-09-730-763-4
; Sequence 4, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIOUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahaw, Garrett &
; ADDRESSEE: Dunner, L.L.P
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
```

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;
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-730-763-4

Query Match      13.9%; Score 267; DB 9; Length 338;
Best Local Similarity 25.6%; Pred. No. 9.3e-17;
Matches 84; Conservative 54; Mismatches 128; Indels 62; Gaps 11;

QY 19 MPPEVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVKEQWQDFLPDPASDG--- 75
Db 1 MSAKLTDLQLLHELEP-----VVEKYLNRHLSMH-----KPNPHDYI--PWSGKNY 46

QY 76 -----FDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQ---TMLNTLDGVYRDET 125
Db 47 YALGGQDMDPDQSKLSVQAQ-----VAMQNLVTEEDNLPVSHREIAMNMGMG----- 94

QY 126 GASPTSWAIWTRAWTAENRHGDLNKLKLYLSGRVDMRQIEKTIQVILGSGMDPRTENS 185
Db 95 -----AWQVWNRWTAENRHGIALRDYLVVTRSVDPVELEKRLLEVNRGFSQGNHOG 149

QY 186 YL-----GFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKHEHAYTK 238
Db 150 HYFAESLTDSLVVSVFQELATRISHRNT---GKACNDPVADQLMAKISADENLHMIFYRD 206

QY 239 IVKLEIFDDPGVILAFADAMRRKISKMPAHLMYDGRDNDLFDHFSAVAQRUGVYTKDYA 298
Db 207 VSEAADFVFN-----QAMKSLHLTLSHFQMPGFQVPEFRKAVVIAVGVDYDRIHL 259

QY 299 D-TLEFLVGRWKVDKLTGLTSAEGOKAOD 325
Db 260 DEVVMPVLKKWCIFEREDFTGEGAKLKD 287

RESULT 14
US-09-730-763-37
; Sequence 37, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIOUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahaw, Garrett &
; ADDRESSEE: Dunner, L.L.P
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
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[illegible]

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:07:57 ; Search time 19 Seconds  
(without alignments)  
562.133 Million cell updates/sec

Title: US-10-017-145-1  
Perfect score: 1916  
Sequence: 1 ASTLKSKEVENLKPFMP.....RAKEAPMPFISWIFDROVKL 363

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1916	100.0	396	1	US-08-539-798-3
2	1916	100.0	396	1	US-08-329-560-3
3	1916	100.0	396	1	US-08-471-791-16
4	1916	100.0	396	4	US-08-926-522-4
5	1916	100.0	396	5	PCT-US91-01746-16
6	1753	91.5	391	1	US-07-995-657-6
7	1753	91.5	391	1	US-08-474-587-6
8	1752	91.4	396	1	US-08-471-791-13
9	1752	91.4	396	4	US-08-926-522-2
10	1752	91.4	396	5	PCT-US91-01746-13
11	1698	88.6	398	1	US-08-471-791-20
12	1698	88.6	398	4	US-08-926-522-6
13	1698	88.6	398	5	PCT-US91-01746-20
14	1316	68.7	385	1	US-08-539-798-4
15	1316	68.7	385	1	US-08-329-560-4
16	1261	65.8	387	1	US-08-539-798-2
17	1261	65.8	387	1	US-08-329-560-2
18	1218	63.6	368	2	US-08-869-137-2
19	291	15.2	54	3	US-08-917-299-12
20	291	15.2	54	3	US-08-917-299-16
21	291	15.2	54	4	US-09-422-662-12
22	291	15.2	54	4	US-09-422-662-16
23	286	14.9	54	3	US-08-917-299-13
24	286	14.9	54	4	US-09-422-662-13
25	283	14.8	54	3	US-08-917-299-15
26	283	14.8	54	4	US-09-422-662-15
27	276	14.4	54	3	US-08-917-299-18

28	276	14.4	54	4	US-09-422-662-18	Sequence 18, Appl
29	273	14.2	52	3	US-08-917-299-27	Sequence 27, Appl
30	273	14.2	52	4	US-09-422-662-27	Sequence 27, Appl
31	273	14.2	56	1	US-08-471-791-2	Sequence 2, Appl
32	273	14.2	56	5	PCT-US91-01746-2	Sequence 2, Appl
33	271	14.1	52	3	US-08-917-299-31	Sequence 31, Appl
34	271	14.1	52	4	US-09-422-662-31	Sequence 31, Appl
35	271	14.1	54	3	US-08-917-299-17	Sequence 17, Appl
36	271	14.1	54	4	US-09-422-662-17	Sequence 17, Appl
37	270	14.1	54	3	US-08-917-299-14	Sequence 14, Appl
38	270	14.1	54	4	US-09-422-662-14	Sequence 14, Appl
39	267	13.9	57	1	US-08-471-791-7	Sequence 7, Appl
40	267	13.9	57	5	PCT-US91-01746-7	Sequence 7, Appl
41	267	13.9	338	3	US-08-917-299-4	Sequence 4, Appl
42	267	13.9	338	3	US-08-917-299-37	Sequence 37, Appl
43	267	13.9	338	4	US-09-422-662-4	Sequence 4, Appl
44	267	13.9	338	4	US-09-422-662-37	Sequence 37, Appl
45	262	13.7	52	3	US-08-917-299-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-08-539-798-3  
; Sequence 3, Application US/08539798  
; Patent No. 5614400  
; GENERAL INFORMATION:  
; APPLICANT: CAHOON, Edgar B.  
; APPLICANT: OHLROGEE, John B.  
; TITLE OF INVENTION: Methods and Compositions Relating to  
; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Pioneer Hi-Bred International, Inc.  
; STREET: 700 Capital Square, 400 Locust Street  
; CITY: Des Moines  
; STATE: Iowa  
; COUNTRY: US  
; ZIP: 50309  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/539,798  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/329,560  
; FILING DATE: 26-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Yates, Michael E.  
; REGISTRATION NUMBER: 36,063  
; REFERENCE/DOCKET NUMBER: 028405  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (515) 248-4800  
; TELEFAX: (515) 248-4844  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-539-798-3  
Query Match 100.0%; Score 1916; DB 1; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2, 2e-180;  
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ASTLKSKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVK 60  
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Db 34 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVEK 93
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Db 94 CWOQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQYTNLTLDG 153
Qy 121 VRDETASPTSWAITWTRAWTAENRHDLLNKLYLSGRVDMRQIEKTIQYLGSGMDPR 180
Db 154 VRDETASPTSWAITWTRAWTAENRHDLLNKLYLSGRVDMRQIEKTIQYLGSGMDPR 213
Qy 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 240
Db 214 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 273
Qy 241 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHFSAVAQRLGVYTTAKDYADI 300
Db 274 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHFSAVAQRLGVYTTAKDYADI 333
Qy 301 LEFLVGRWKVDKLTGLSAEGQKAQDYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 360
Db 334 LEFLVGRWKVDKLTGLSAEGQKAQDYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 393
Qy 361 VKL 363
Db 394 VKL 396

RESULT 2
US-08-329-560-3
; Sequence 3, Application US/08329560
; Patent No. 5654402
; GENERAL INFORMATION:
; APPLICANT: CAHOON, Edgar B.
; APPLICANT: OHLROGEE, John B.
; TITLE OF INVENTION: Methods and Compositions Relating to
; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: US
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,560
; FILING DATE: 26-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Yates, Michael E.
; REGISTRATION NUMBER: 36,063
; REFERENCE/DOCKET NUMBER: 0284US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 3:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-329-560-3
Query Match 100.0%; Score 1916; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 2,2e-180;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVEK 60

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Db 34 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVEK 93
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Db 94 CWOQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQYTNLTLDG 153
Qy 121 VRDETASPTSWAITWTRAWTAENRHDLLNKLYLSGRVDMRQIEKTIQYLGSGMDPR 180
Db 154 VRDETASPTSWAITWTRAWTAENRHDLLNKLYLSGRVDMRQIEKTIQYLGSGMDPR 213
Qy 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 240
Db 214 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 273
Qy 241 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHFSAVAQRLGVYTTAKDYADI 300
Db 274 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHFSAVAQRLGVYTTAKDYADI 333
Qy 301 LEFLVGRWKVDKLTGLSAEGQKAQDYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 360
Db 334 LEFLVGRWKVDKLTGLSAEGQKAQDYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 393
Qy 361 VKL 363
Db 394 VKL 396

RESULT 3
US-08-471-791-16
; Sequence 16, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knauf, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoftword 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762,762
; FILING DATE: 16-SEPT-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth

```

REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
NAME: Carl J. Schwedler  
REGISTRATION NUMBER: 36,924  
REFERENCE/DOCKET NUMBER: CGNE 69-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
TELEX: 350370 CGNE  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-791-16

Query Match 100.0%; Score 1916; DB 1; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.2e-180;  
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTLSGSGKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60  
DB 34 ASTLSGSGKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93

QY 61 CWOQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 120  
DB 94 CWOQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 153

QY 121 VRDETGAPTSNAIWTAWTAENRHGDLNKKYLYLSGRVDMRQIEKTIQYILIGSGMDPR 180  
DB 154 VRDETGAPTSNAIWTAWTAENRHGDLNKKYLYLSGRVDMRQIEKTIQYILIGSGMDPR 213

QY 181 TNSPYLGFITYSFQERATFISHGNTARQAKHEGDIKLAQICCTAADEKRHETAYTKIV 240  
DB 214 TNSPYLGFITYSFQERATFISHGNTARQAKHEGDIKLAQICCTAADEKRHETAYTKIV 273

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DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYAKDYADI 333

QY 301 LEFLVGRWKVDKLTGLSAGQKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 360  
DB 334 LEFLVGRWKVDKLTGLSAGQKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 393

RESULT 4  
US-08-926-522-4  
Sequence 4, Application US/08926522  
Patent No. 6426447  
GENERAL INFORMATION:  
APPLICANT: Vic C. Knauf  
APPLICANT: Gregory A. Thompson  
TITLE OF INVENTION: PLANT SEED OILS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.1  
SOFTWARE: Microsoft Word 5.1(a)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/926,522  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,173  
FILING DATE: 2-June-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth Lassen  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
NAME: Carl J. Schwedler  
REGISTRATION NUMBER: 36,924  
REFERENCE/DOCKET NUMBER: CGNE DES  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-926-522-4

Query Match 100.0%; Score 1916; DB 4; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.2e-180;  
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTLSGSGKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60  
DB 34 ASTLSGSGKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93

QY 61 CWOQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 120  
DB 94 CWOQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 153

QY 121 VRDETGAPTSNAIWTAWTAENRHGDLNKKYLYLSGRVDMRQIEKTIQYILIGSGMDPR 180  
DB 154 VRDETGAPTSNAIWTAWTAENRHGDLNKKYLYLSGRVDMRQIEKTIQYILIGSGMDPR 213

QY 181 TNSPYLGFITYSFQERATFISHGNTARQAKHEGDIKLAQICCTAADEKRHETAYTKIV 240  
DB 214 TNSPYLGFITYSFQERATFISHGNTARQAKHEGDIKLAQICCTAADEKRHETAYTKIV 273

QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYAKDYADI 300  
DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYAKDYADI 333

QY 301 LEFLVGRWKVDKLTGLSAGQKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 360  
DB 334 LEFLVGRWKVDKLTGLSAGQKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 393

QY 361 VKL 363  
DB 394 VKL 396

RESULT 5  
PCT-US91-01746-16  
Sequence 16, Application PC/TUS9101746  
GENERAL INFORMATION:  
APPLICANT: Thompson, Gregory A  
APPLICANT: Knauf, Vic C  
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: California  
COUNTRY: USA  
ZIP: 95616

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 19910314
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELEX: 350370 CGNE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-01746-16

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Query Match 100.0%; Score 1916; DB 5; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-180;  
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 34 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93

Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120
Db 94 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153

Qy 121 VRDETASPTSWA1WTRAWTAENRHGDLNKNLYLSGRVDMROIEKTIQVLYIGSGMDPR 180
Db 154 VRDETASPTSWA1WTRAWTAENRHGDLNKNLYLSGRVDMROIEKTIQVLYIGSGMDPR 213

Qy 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 240
Db 214 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 273

Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGYVTAKDYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGYVTAKDYADI 333

Qy 301 LEFLVGRKWKVDKLTGLSAGQAKADYVCRPLPRRLRLEERAQGRAKEAPTWPFSWIFDRQ 360
Db 334 LEFLVGRKWKVDKLTGLSAGQAKADYVCRPLPRRLRLEERAQGRAKEAPTWPFSWIFDRQ 393

Qy 361 VKL 363
Db 394 VKL 396

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RESULT 6  
 us-07-995-657-6  
 ; Sequence 6, Application US/07995657  
 ; Patent No. 5443974  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hitz, William D.

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; APPLICANT: Yadav, Narendra S.
; APPLICANT: Perez, Grau, Luis
; TITLE OF INVENTION: Nucleotide Sequence of
; TITLE OF INVENTION: Soybean Stearoyl-ACP
; TITLE OF INVENTION: Desaturase CDNA
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/995,657
; FILING DATE: 19921211
; FILING DATE: C) CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: GEIGER, KATHLEEN W.
; REGISTRATION NUMBER: 35,880
; REFERENCE/DOCKET NUMBER: BB_1022-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-995-657-6

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Query Match 91.5%; Score 1753; DB 1; Length 391;  
 Best Local Similarity 89.8%; Pred. No. 2.4e-164;  
 Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

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Qy 1 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 29 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 88

Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120
Db 89 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 148

Qy 121 VRDETASPTSWA1WTRAWTAENRHGDLNKNLYLSGRVDMROIEKTIQVLYIGSGMDPR 180
Db 149 VRDETASPTSWA1WTRAWTAENRHGDLNKNLYLSGRVDMROIEKTIQVLYIGSGMDPR 208

Qy 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 240
Db 209 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 268

Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGYVTAKDYADI 300
Db 269 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGYVTAKDYADI 328

Qy 301 LEFLVGRKWKVDKLTGLSAGQAKADYVCRPLPRRLRLEERAQGRAKEAPTWPFSWIFDRQ 360
Db 329 LEFLVGRKWKVDKLTGLSAGQAKADYVCRPLPRRLRLEERAQGRAKEAPTWPFSWIFDRQ 388

Qy 361 VKL 363
Db 361 VKL 363

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Db 389 VLL 391
RESULT 7
US-08-474-587-6
; Sequence 6, Application US/08474587
; Patent No. 5760206
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Perez-Grau, Luis
; TITLE OF INVENTION: Nucleotide Sequence of
; Patent No. 5760206
; TITLE OF INVENTION: Soybean Stearoyl-ACP
; TITLE OF INVENTION: Desaturase cDNA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474.587
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: SIEGELL, BARBARA C.
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB_1022-C
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-587-6
Query Match 91.5%; Score 1753; DB 1; Length 391;
Best Local Similarity 89.8%; Pred. No. 2.4e-164;
Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;
QY 1 ASTLKSKEVENLKKPMPPEHVHVQVTHSMPPKQIEIFKSLDNWAEENILVHLKPVKE 60
Db 29 ASTLRSKSEVENIKKPPFPPEHVHVQVTHSMPPKQIEIFKSLDWDQONILTHLKPVEK 88
QY 61 CWQPDQFLPDASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLDG 120
Db 89 CWQPDQFLPDSSDGFEEQVKELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLDG 148
QY 121 VRDETGAFTSWAIWTRAWTAENRHGDLNLYLXSGRVDVRQIEKTIQYILIGSGMDPR 180
Db 149 VRDETGAFTSWAIWTRAWTAENRHGDLNLYLXSGRVDVRQIEKTIQYILIGSGMDPR 208
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKRHETAYTKIV 240
Db 209 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGMIASDEKRHETAYTKIV 268
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QY 241 EKLFEIDPDGTVLAFADMMRRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYTKADYADI 300
Db 269 EKLFEVDPDGTVMAFADMMRRKKIAMPAHLMYDGRDNLDFNYSAVAQRIGVYTKADYADI 328
QY 301 LEFLVGRWKVKLTGLSABGQAAQDYVCRLPPIRRLERAAQRAKEAETMPFSWIFDRQ 360
Db 329 LEFLVGRWKVEQTLGLSGEGRKAQYVCGLPPIRRLERAAQARGKESSTLAKFSWIHDRE 388
QY 361 VKL 363
Db 389 VLL 391
RESULT 8
US-08-471-791-13
; Sequence 13, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knauf, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 69-5
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELEX: 350370 CGNE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein  
US-08-471-791-13

Query Match 91.4%; Score 1752; DB 1; Length 396;  
Best Local Similarity 90.1%; Pred. No. 3e-164;  
Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

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QY 1 ASTLKSGKEVENLKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPEVK 60
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Db 34 ASTLGSSTPKVDNAKKFPQPPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPEVK 93
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CWPQDFLPDPASGDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTLDG 120
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 94 CWOAQDFLPDPASGDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTLDG 153
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 VRDETASPTSWAIVTAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLIIGSGMDPR 180
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Db 154 VRDETASLTPMAVWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLIIGSGMDPR 213
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QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHGDIKLAQICGTIAADEKRHHETATYKIV 240
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAKHGDIKLAQICGTIAADEKRHHETATYKIV 273
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAORGLVYTKADYADI 300
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAORGLVYTKADYADI 333
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 LEFLVGRWKVDKLTGLSNEGOKAODYVCRLLPPIRRRLLEERAQGRKEAPTMPFSWIFDRQ 360
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 334 LEFLVGRWKVADLTGLSGEGRKAQDYVCGLLPPIRRRLLEERAQGRKEAPTMPFSWIFDRQ 393
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 VKL 363
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Db 394 VKL 396
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RESULT 9

US-08-926-522-2  
; Sequence 2, Application US/08926522  
; Patent No. 6426447  
; GENERAL INFORMATION:  
; APPLICANT: Vic C. Knauf  
; APPLICANT: Gregory A. Thompson  
; TITLE OF INVENTION: PLANT SEED OILS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calgene, Inc.  
; STREET: 1920 Fifth Street  
; CITY: Davis  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 95616  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.1  
; SOFTWARE: Microsoft Word 5.1(a)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/926,522  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/458,173  
; FILING DATE: 2-June-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth Lassen  
; REGISTRATION NUMBER: 31,845  
; NAME: Donna E. Scherer  
; REGISTRATION NUMBER: 34,719  
; NAME: Carl J. Schwedler  
; REGISTRATION NUMBER: 36,924  
; REFERENCE/DOCKET NUMBER: CGNE DES  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (916) 753-6313  
; TELEFAX: (916) 753-1510  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-926-522-2

Query Match 91.4%; Score 1752; DB 4; Length 396;  
Best Local Similarity 90.1%; Pred. No. 3e-164;  
Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

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QY 1 ASTLKSGKEVENLKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPEVK 60
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Db 34 ASTLGSSTPKVDNAKKFPQPPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPEVK 93
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CWPQDFLPDPASGDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTLDG 120
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 94 CWOAQDFLPDPASGDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTLDG 153
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 VRDETASPTSWAIVTAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLIIGSGMDPR 180
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154 VRDETASLTPMAVWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLIIGSGMDPR 213
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHGDIKLAQICGTIAADEKRHHETATYKIV 240
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAKHGDIKLAQICGTIAADEKRHHETATYKIV 273
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAORGLVYTKADYADI 300
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAORGLVYTKADYADI 333
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 LEFLVGRWKVDKLTGLSNEGOKAODYVCRLLPPIRRRLLEERAQGRKEAPTMPFSWIFDRQ 360
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 334 LEFLVGRWKVADLTGLSGEGRKAQDYVCGLLPPIRRRLLEERAQGRKEAPTMPFSWIFDRQ 393
    ||||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 VKL 363
    |||
Db 394 VKL 396
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RESULT 10

PCT-US91-01746-13  
; Sequence 13, Application PC/TUS9101746  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Gregory A  
; APPLICANT: Knauf, Vic C  
; TITLE OF INVENTION: Plant Desaturases-Compositions and Uses  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calgene, Inc.  
; STREET: 1920 Fifth Street  
; CITY: Davis  
; STATE: California  
; COUNTRY: USA  
; ZIP: 95616  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 6.0.7  
; SOFTWARE: MicrosoftWord 4.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/01746  
; FILING DATE: 19910314  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/615,784  
; FILING DATE: 14-NOV-1990  
; APPLICATION NUMBER: 07/567,373  
; FILING DATE: 13-AUG-1990  
; APPLICATION NUMBER: 07/494,106

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; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELEX: 350370 CGNE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-01746-13

Query Match          91.4%; Score 1752; DB 5; Length 396;
Best Local Similarity 90.1%; Pred. No. 3e-164;
Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 ASTLKSGSKEVENLKKPFPPREVHVQVTHSMPPQKIEIFKSLDNWAENILVHLKPVKEK 60
DB 34 ASTLGSSTPKVDNAKKPFQPPREVHVQVTHSMPPQKIEIFKSIEGWAENILVHLKPVKEK 93
QY 61 CWQPDFLPDPSGDFDQVRELREAKEIPDDYFVVLVGDMLTEALPTQTMNTLDG 120
DB 94 CWAQDFLPDPASEGDFEQVKELRAAKEIPDDYFVVLVGDMLTEALPTQTMNTLDG 153
QY 121 VRDETGAFTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQTEKTIQYLLIGSGMDPR 180
DB 154 VRDETGASLTPWAVWTRAWTAENRHGDLNKKLYLSGRVDMRQTEKTIQYLLIGSGMDPR 213
QY 181 TENSPLYGFTYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRRHETAYTKIV 240
DB 214 TENSPLYGFTYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRRHETAYTKIV 273
QY 241 EKLFFIDPDGTVLAFADMMRKKSMPAHLMYDGRDNLDFHFSAVAQRUGVYTAQDYADI 300
DB 274 EKLFFIDPDGTVLAFADMMRKKSMPAHLMYDGRDNLDFHFSAVAQRUGVYTAQDYADI 333
QY 301 LEFLYGRWKVDKLTGLSAGQKAQDYVCRLLPPIRRLEERAQRAKEAFTMPFSWIFDRQ 360
DB 334 LEFLYGRWKVDKLTGLSAGQKAQDYVCRLLPPIRRLEERAQRAKEAFTMPFSWIFDRQ 393
QY 361 VKL 363
DB 394 VKL 396

RESULT 11
US-08-471-791-20
; Sequence 20, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knauf, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
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; SOFTWARE: MicrosoftWord 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762,762
; FILING DATE: 16-SEPT-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; APPLICATION DATA:
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 69-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELEX: 350370 CGNE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-791-20

Query Match          88.6%; Score 1698; DB 1; Length 398;
Best Local Similarity 88.2%; Pred. No. 6.3e-159;
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 8 SKEVENLKKPFPPREVHVQVTHSMPPQKIEIFKSLDNWAENILVHLKPVKEKWPQDF 67
DB 43 SKEVESLKKPFPPREVHVQVTHSMPPQKIEIFKSMEDWAEQNLLTQLKDVKEKSWQPDF 102
QY 68 LPDPASDGFDEQVRELREAKEIPDDYFVVLVGDMLTEALPTQTMNTLDGVRDETGA 127
DB 103 LPDPASDGFDEQVRELREAKEIPDDYFVVLVGDMLTEALPTQTMNTLDGVRDETGA 162
QY 128 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYLLIGSGMDPRTEENPYL 187
DB 163 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYLLIGSGMDPRTEENPYL 222
QY 188 GFITYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRRHETAYTKIVKLEFID 247
DB 223 GFITYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRRHETAYTKIVKLEFID 282
QY 248 PDGTVLAFADMMRKKSMPAHLMYDGRDNLDFHFSAVAQRUGVYTAQDYADILEFLVGR 307
DB 283 PDGTVLAFADMMRKKSMPAHLMYDGRDNLDFHFSAVAQRUGVYTAQDYADILEFLVGR 342
QY 308 WKVVDKLTGLSAGQKAQDYVCRLLPPIRRLEERAQRAKEAFTMPFSWIFDRQVKL 363
DB 343 WKIESLTGLSAGQKAQDYVCRLLPPIRRLEERAQRAKEAFTMPFSWIFDRQVKL 398

RESULT 12
US-08-926-522-6
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: Sequence 6, Application US/08926522
: Patent No. 6426447
: GENERAL INFORMATION:
: APPLICANT: Vic C. Knauf
: TITLE OF INVENTION: PLANT SEED OILS
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Calgene, Inc.
: STREET: 1920 Fifth Street
: CITY: Davis
: STATE: CA
: COUNTRY: USA
: ZIP: 95616
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
: OPERATING SYSTEM: Macintosh 7.1
: SOFTWARE: Microsoft Word 5.1(a)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/926,522
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/458,173
: FILING DATE: 2-June-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Elizabeth Lassen
: REGISTRATION NUMBER: 31,845
: NAME: Donna E. Scherer
: REGISTRATION NUMBER: 34,719
: NAME: Carl J. Schwedler
: REGISTRATION NUMBER: 36,924
: REFERENCE/DOCKET NUMBER: CGNE DES
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (916) 753-6313
: TELEFAX: (916) 753-1510
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 398 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-926-522-6

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Query Match      88.6%; Score 1698; DB 4; Length 398;
Best Local Similarity 88.2%; Pred. No. 6.3e-159;
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

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QY 68 LPDPASGDFEQVRELREARAKEIPDDYFVVLVGMITEEALPTYQTMNLTLDGVRDETGA 127
Db 103 LPDPASGDFEQVRELREARAKEIPDDYFVVLVGMITEEALPTYQTMNLTLDGVRDETGA 162
QY 128 SPTSWAIWTRAWTAENRHHGDLNKKYLYLSGRVDMRQIEKTIQYLGSGMDPRTEENPYL 187
Db 163 SPTSWAIWTRAWTAENRHHGDLNKKYLYLSGRVDMRQIEKTIQYLGSGMDPRTEENPYL 222
QY 188 GFYITSFQERATFISHGNTARAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLEFID 247
Db 223 GFYITSFQERATFISHGNTARAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLEFID 282
QY 248 PDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADILEFLVGR 307
Db 283 PDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADILEFLVGR 342
QY 308 WKYDKLTLGSAEQKADQYVCRPLPRIRRLREERAQRAKEAPTMFSPWIFDROVKL 363
Db 343 WKIESUTGLSGEKNKAQYELCGLTPRIRRLDERAQAQRAKKGKVPFSPWIFDROVKL 398

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RESULT 13
PCT-US91-01746-20
: Sequence 20, Application PC/TUS9101746
: GENERAL INFORMATION:
: APPLICANT: Thompson, Gregory A
: APPLICANT: Knauf, Vic C
: TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Calgene, Inc.
: STREET: 1920 Fifth Street
: CITY: Davis
: STATE: California
: COUNTRY: USA
: ZIP: 95616
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
: OPERATING SYSTEM: Macintosh 6.0.7
: SOFTWARE: Microsoft Word 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/01746
: FILING DATE: 19910314
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/615,784
: FILING DATE: 14-NOV-1990
: APPLICATION NUMBER: 07/567,373
: FILING DATE: 13-AUG-1990
: APPLICATION NUMBER: 07/494,106
: FILING DATE: 16-MAR-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Lassen, Elizabeth
: REGISTRATION NUMBER: 31,845
: NAME: Donna E. Scherer
: REGISTRATION NUMBER: 34,719
: REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (916) 753-6313
: TELEFAX: (916) 753-1510
: TELEX: 350370 CGNE
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 398 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US91-01746-20

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Query Match      88.6%; Score 1698; DB 5; Length 398;
Best Local Similarity 88.2%; Pred. No. 6.3e-159;
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

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QY 8 SKEVENLKPFMPREVVHVVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVKWCWQPDF 67
Db 43 SKEVESLKPFPTPPKEVHVQVLSHMPQKTEIFKSMEDWAEQNLLTLQKDKVKSQWQPDF 102
QY 68 LPDPASGDFEQVRELREARAKEIPDDYFVVLVGMITEEALPTYQTMNLTLDGVRDETGA 127
Db 103 LPDPASGDFEQVRELREARAKEIPDDYFVVLVGMITEEALPTYQTMNLTLDGVRDETGA 162
QY 128 SPTSWAIWTRAWTAENRHHGDLNKKYLYLSGRVDMRQIEKTIQYLGSGMDPRTEENPYL 187
Db 163 SPTSWAIWTRAWTAENRHHGDLNKKYLYLSGRVDMRQIEKTIQYLGSGMDPRTEENPYL 222
QY 188 GFYITSFQERATFISHGNTARAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLEFID 247
Db 223 GFYITSFQERATFISHGNTARAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLEFID 282
QY 248 PDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADILEFLVGR 307
Db 283 PDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADILEFLVGR 342

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Db 257 YTKIVEKLAETIDPDTTVIAFSDMMRKKIOMPAHAMYDGSDDMLFKHFTAVSQOIGVYSAW 316  
Qy 296 DYADILEFLVGRWKVDKLTGLSAGOKAODYVCLPPRIERLEERAQGRAKEAPTMP--F 353  
Db 317 DYCDDLDLFLVDKWNVAKMTGLSGEGRKAOEYVCSLAAKIRRVEEKVOGREKKA-VLPVAF 375  
Qy 354 SWIFDROV 361  
Db 376 SWIFNROI 383

Search completed: March 7, 2003, 03:11:02  
Job time : 20 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2003, 03:03:42 ; Search time 39 seconds  
(without alignments)  
1240.256 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKSQSGKEVNLKKPFMP.....RAKEAPTMPFSWIFDROVKL 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID22/qcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1916	100.0	363	22	AA48199
2	1916	100.0	396	12	AA44350
3	1903	99.3	396	12	AA14189
4	1753	91.5	391	13	AA20011
5	1753	91.5	391	19	AA37939
6	1752	91.4	396	12	AA14188
7	1752	91.4	396	13	AA22048
8	1752	91.4	396	15	AA54033
9	1752	91.4	396	19	AA44349
10	1733	90.4	401	21	AA29699

11	1733	90.4	401	23	ABB92108
12	1733	90.4	401	23	ABB07379
13	1721	89.8	391	16	AA82024
14	1698	88.6	398	12	AA14190
15	1698	88.6	398	18	AA14798
16	1698	88.6	398	19	AA44351
17	1694	88.4	401	18	AA14797
18	1674	87.4	399	15	AA47876
19	1639.5	85.6	393	18	AA49508
20	1639.5	85.6	393	21	AA46887
21	1637	85.4	396	22	AAE13419
22	1636.5	85.4	393	21	AA46888
23	1616.5	84.4	392	21	AA43284
24	1614	84.2	332	21	AA22118
25	1614	84.2	332	21	AA229700
26	1614	84.2	332	21	AA45764
27	1600.5	83.5	394	21	AA45804
28	1600.5	83.5	396	21	AA45803
29	1600.5	83.5	396	23	ABB2182
30	1600.5	83.5	439	21	AA45802
31	1583	82.6	390	17	AA46249
32	1577	82.3	392	21	AA43285
33	1557	81.3	321	21	AA22119
34	1557	81.3	321	21	AA229701
35	1557	81.3	321	21	AA45765
36	1529.5	79.8	391	21	AA45809
37	1529.5	79.8	393	21	AA45808
38	1529.5	79.8	395	21	AA45807
39	1526.5	79.7	394	23	ABB93501
40	1411.5	73.7	414	22	AA80920
41	1380	72.0	411	23	ABB2180
42	1358	70.9	401	23	ABB3500
43	1351	70.5	396	23	ABB2181
44	1318	68.8	391	23	ABB91264
45	1317	68.7	385	16	AA46578

#### ALIGNMENTS

RESULT 1  
AAB48199  
ID AAB48199 standard; Protein; 363 AA.

AC AAB48199;

DT 02-APR-2001 (first entry)

XX Mature castor enzyme.

KW Castor; delta9-18:0-acyl carrier protein desaturase; ACP; enzyme;  
KW vegetable oil; fatty acid; nutrition; plant oil; mutant.

OS Ricinus communis.

XX Key Location/Qualifiers

FT Misc-difference 114 /note= "can be substituted by Ala"

FT Misc-difference 117 /note= "can be substituted by Arg"

FT Misc-difference 118 /note= "can be substituted by Gly"

FT Misc-difference 179 /note= "can be substituted by Val"

FT Misc-difference 181 /note= "can be substituted by Val"

FT Misc-difference 188 /note= "can be substituted by Leu"

XX WO200075170-A1.

XX 14-DEC-2000.

XX

PF 08-JUN-2000; 2000WO-US15741.  
 XX  
 PR 09-JUN-1999; 99US-0328550.  
 XX  
 PA (BROO-) BROOKHAVEN SCI ASSOC LLC.  
 XX  
 PI Shanklin J;  
 XX  
 DR WPI; 2001-091202/10.  
 DR N-PSDB; AAC84531.  
 XX  
 PT New mutant castor Delta9-18:0-Acyl Carrier Protein desaturase, useful  
 PT in producing commercially valuable products, e.g. vegetable oils useful  
 PT in human nutrition or as industrial chemicals  
 XX  
 PS Examples; Fig 1; 53pp; English.  
 XX  
 CC The invention relates to a new mutant castor Delta9-18:0-acyl carrier  
 CC protein (ACP) desaturase that has one or more amino acid substitutions  
 CC selected from: (a) Ala for Met at residue 114; (b) Arg for Thr at residue  
 CC 117; (c) Gly for Leu at residue 118; (d) Val for Pro at residue 179; (e)  
 CC Val for Thr at residue 181; (f) Leu for Gly at residue 188; and (g) Phe  
 CC Val for Thr at residue 181. The mutant castor Delta9-18:0-ACP desaturase is  
 CC useful in producing commercially useful products, such as vegetable oils  
 CC rich in monounsaturated fatty acids. Such vegetable oils are important in  
 CC human nutrition and can be used as renewable sources of industrial  
 CC chemicals. A method for specifically altering a function of a protein  
 CC through directed mutagenesis is also provided. The method can be used  
 CC altering enzymatic functions, binding functions or structural functions  
 CC of the castor desaturase enzyme. The method is also useful for  
 CC manipulating the physical properties and commercial uses of conventional  
 CC plant oils. The present sequence represents the mature castor enzyme.  
 XX  
 SQ Sequence 363 AA;

Query Match 100.0%; Score 1916; DB 22; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-171;  
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60  
 DB 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60  
 QY 61 CWPQDFLPDPASDGFQVRELREAKEIPDDYFVVLVGMITEEALPTVQTMINTLDG 120  
 DB 61 CWPQDFLPDPASDGFQVRELREAKEIPDDYFVVLVGMITEEALPTVQTMINTLDG 120  
 QY 121 VRDETGASPTSWA IWTAWTAENRHGDLNKLKYL LSGRVDMMROI EKT IQLIGSGMDPR 180  
 DB 121 VRDETGASPTSWA IWTAWTAENRHGDLNKLKYL LSGRVDMMROI EKT IQLIGSGMDPR 180  
 QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTTAADEKRRHETAYTKIV 240  
 DB 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTTAADEKRRHETAYTKIV 240  
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTAQDYADI 300  
 DB 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTAQDYADI 300  
 QY 301 LEFLVGRWKVDKLTLSAEGOKAODYVCLRPPIRRLLEERAQGRAKEAPTWPFSWIFDRQ 360  
 DB 301 LEFLVGRWKVDKLTLSAEGOKAODYVCLRPPIRRLLEERAQGRAKEAPTWPFSWIFDRQ 360  
 QY 361 VKL 363  
 DB 361 VKL 363

RESULT 2  
 AAW44350  
 ID AAW44350 standard; Protein; 396 AA.  
 XX  
 AC AAW44350;

XX 28-MAY-1998 (first entry)  
 DT  
 XX Ricinus communis desaturase from clone pCGN3230.  
 DE  
 XX Ricinus communis; castor bean; delta-9 desaturase; oilseed;  
 KW fatty acid saturation.  
 KW  
 XX Ricinus communis.  
 OS  
 XX US5723595-A.  
 PN  
 XX 03-MAR-1998.  
 PD  
 XX 06-JUN-1995; 95US-0471791.  
 PF  
 XX 16-SEP-1991; 91US-0762762.  
 PR  
 PR 16-MAR-1990; 90US-0494106.  
 PR  
 PR 13-AUG-1990; 90US-0567373.  
 PR  
 PR 14-NOV-1990; 90US-0615784.  
 PR  
 PR 14-MAR-1991; 91WO-US01746.  
 PR  
 PR 06-JUN-1995; 95US-0471791.  
 XX  
 PA (CALJ ) CALGENE INC.  
 XX  
 XX Knauf VC, Thompson GA;  
 PI  
 XX WPI; 1998-178544/16.  
 XX  
 DR N-PSDB; AAV15252.  
 DR  
 DR  
 XX DNA encoding plant delta-9 desaturase protein - having amino acid  
 PT sequence of Carthamus tinctorius desaturase, useful for, e.g.  
 PT producing oil-seeds with modified levels of fatty acid saturation  
 PT  
 XX  
 PS Claim 7; Column 59-60; 87pp; English.  
 XX  
 CC The present sequence represents a Ricinus communis desaturase from  
 CC clone pCGN3230. The present invention describes a recombinant DNA  
 CC construct comprising a DNA sequence encoding a plant Delta-9 desaturase  
 CC protein. The present invention also provides a method of modifying fatty  
 CC acid composition in a host plant cell from a given fatty acid saturation  
 CC to a different fatty acid saturation, comprising growing a host plant  
 CC cell containing a recombinant DNA sequence which encodes a plant  
 CC desaturase under the control of regulatory elements functional in the  
 CC plant cell during lipid accumulation. Also, oilseeds having a modified  
 CC level of fatty acid saturation and oils produced from such oilseeds.  
 XX  
 SQ Sequence 396 AA;  
 Query Match 100.0%; Score 1916; DB 19; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-171;  
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60  
 DB 34 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93  
 QY 61 CWPQDFLPDPASDGFQVRELREAKEIPDDYFVVLVGMITEEALPTVQTMINTLDG 120  
 DB 94 CWPQDFLPDPASDGFQVRELREAKEIPDDYFVVLVGMITEEALPTVQTMINTLDG 153  
 QY 121 VRDETGASPTSWA IWTAWTAENRHGDLNKLKYL LSGRVDMMROI EKT IQLIGSGMDPR 180  
 DB 154 VRDETGASPTSWA IWTAWTAENRHGDLNKLKYL LSGRVDMMROI EKT IQLIGSGMDPR 213  
 QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTTAADEKRRHETAYTKIV 240  
 DB 214 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTTAADEKRRHETAYTKIV 273  
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTAQDYADI 300  
 DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTAQDYADI 333

```
Qy 301 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 360
|||||
Db 334 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 393
Qy 361 VKL 363
|||
Db 394 VKL 396

RESULT 3
ID AAR14189 standard; Protein; 396 AA.
XX AC AAR14189;
XX DT 11-DEC-1991 (first entry)
XX DE R. communis delta9 desaturase from pCGN3230.
XX KW Desaturase; fatty acid; saturation; chill tolerance; lipid;
XX KW herbicide.
XX OS Ricinus communis.
XX PN WO9113972-A.
XX PD 19-SEP-1991.
XX PF 14-MAR-1991; 91WO-U001746.
XX PR 14-NOV-1990; 90US-0615784.
XX PR 16-MAR-1990; 90US-0494106.
XX PR 13-AUG-1990; 90US-0567373.
XX PA (CALG-) CALGENE INC.
XX PI Thompson G, Knauf V;
XX WPI; 1991-295627/40.
XX DR N-PSDB; AAQ13964.
XX DNA encoding a plant desaturase - used for modifying the satd.
XX fatty acid compsn. of plant cells and plant seeds
XX PS Disclosure; Fig 3B; 128pp; English.
XX CC Modification of fatty acid in a plant host cell to a different
XX percentage of fatty acid satn. is possible by growing a host plant
XX cell having integrated into its genome a recombinant DNA sequence
XX encoding this protein, under the control of regulatory elements
XX functional in the plant cell during lipid accumulation, under
XX conditions which will promote the activity of the regulatory elements.
XX By increasing the amt. of desaturase available in plant cells, an
XX increased percentage of unsatd. fatty acids may be provided, using
XX anti-sense technology, the amt. of desaturase can be decreased,
XX resulting in a higher percentage of fatty acids.
XX Using the desaturase gene and derivs. in cells and plants,
XX desirable traits such as chill tolerance may be introduced and
XX environmentally safe herbicide prods. may be provided.
XX See also AAQ13963-69.
SQ Sequence 396 AA;

Query Match 99.3%; Score 1903; DB 12; Length 396;
Best Local Similarity 99.2%; Pred. No. 2.3e-170;
Matches 360; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
|||||
Db 34 ASTLKSGSKEVENLKKPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93
Qy 61 CWOQDFLPDPASGDFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120
|||||
```

```
Db 94 CWOQDFLPDPASGDFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153
Qy 121 VDETGASPTSWAIWTRAWTAENRHGDLNKNYLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180
|||||
Db 154 VGDETGASPTSWAIWTRAWTAENRHGDLNKNYLYLSGRVDMRQIEKTIQYLLIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIV 240
|||||
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRILGVYTAQDYADI 300
|||||
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRILGVYTAQDYADI 333
Qy 301 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 360
|||||
Db 334 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 393
Qy 361 VKL 363
|||
Db 394 VKL 396

RESULT 4
AAR20011
ID AAR20011 standard; Protein; 391 AA.
XX AC AAR20011;
XX DT 31-MAR-1992 (first entry)
XX DE Soybean seed stearyl-ACP desaturase.
XX KW soya bean; plant oil; stearic acid.
XX OS Glycine max strain Cultivar Wye.
XX FH Key
XX FT Peptide 1..32
XX FT /label- transit
XX FT Protein 33..391
XX PN WO9118985-A.
XX PD 12-DEC-1991.
XX PF 16-MAY-1991; 91WO-US03288.
XX PR 25-MAY-1990; 90US-0529049.
XX PA (DUPO ) DU PONT DE NEMOURS CO.
XX PI Hitz WD, Yadav N;
XX WPI; 1992-007469/01.
XX DR N-PSDB; AAQ20187.
XX DNA encoding soybean stearyl-ACP desaturase enzyme and precursor
XX - and chimeric genes, for plant transformation and control of
XX levels of satd. and unsaturated fatty acids in edible oils
XX PS Disclosure; Page 54; 70pp; English.
XX CC Levels of saturated and unsaturated fatty acids can be controlled
XX in plants, e.g. oilseed rape, sunflower, soybean, peanut, etc.,
XX transformed with nucleic acid sequences coding for the expression
XX of this enzyme.
XX See also AAQ20188-Q20190 and AAR20012.
SQ Sequence 391 AA;

Query Match 91.5%; Score 1753; DB 13; Length 391;
Best Local Similarity 89.8%; Pred. No. 2.9e-156;
```

Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

QY 1 ASTLKSKEVENLKPPFPPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60  
 DB 29 ASTLRSGSKEVENIKKPPFTPPREVHVQVTHSMPPQKIEIFKSLDNWADQNILTHLKPVEK 88  
 QY 61 CWPQDFLPDPASDGDGDEQVRELRAKEIPDDYFVVLVGDMMITEALPYQTMNLTLG 120  
 DB 89 CWPQDFLPDPSSDGDGFEQVKELRAKEIPDDYFVVLVGDMMITEALPYQTMNLTLG 148  
 QY 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180  
 DB 149 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 208  
 QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGMIASDEKRHETATYKIV 240  
 DB 209 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGMIASDEKRHETATYKIV 268  
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAQRGLGYTAKDYADI 300  
 DB 269 EKLFEVDPDGTVMAFADMMRKKIKAMPAHLMYDGRDDNLFDFNYSVAQRIGVYTAQDYADI 328  
 QY 301 LEFLVGRWKVDKLTGLSAGOKAQDYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 360  
 DB 329 LEFLVGRWKVEQLTGLSGEGRKAQYVCGLPPIRRLEERAQRAKESSTLKFWSWIHDRE 388  
 QY 361 VKL 363  
 DB 389 VLL 391

RESULT 5  
 AAW37939  
 ID AAW37939 standard; Protein; 391 AA.  
 AC AAW37939;  
 XX 21-AUG-1998 (first entry)  
 DT Amino acid sequence of the soybean seed stearyl-ACP desaturase.  
 DE Soybean stearyl ACP-desaturase; chimeric gene; antisense;  
 KW transformation; saturated fatty acid; unsaturated fatty acid;  
 KW soybean oil; inhibition; polyunsaturate; monosaturate.  
 XX Glycine max.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..32  
 FT /note= "transit peptide"  
 FT Protein 33..391  
 FT /note= "mature protein"  
 XX US5760206-A.  
 XX 02-JUN-1998.  
 XX 07-JUN-1995; 95US-0474587.  
 XX 07-JUN-1995; 95US-0474587.  
 PR 19-MAY-1991; 91WO-US03288.  
 PR 11-DEC-1992; 92US-0995657.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Hitz WD, Perez-Grau L, Yadav NS;  
 XX WPI; 1998-332247/29.  
 DR N-ESDB; AAV29236.  
 XX Nucleic acids encoding soybean seed stearyl-ACP desaturase enzyme -  
 PT are useful for the anti-sense inhibition of the enzyme in  
 PT transformed plant cells

XX Disclosure; Column 43-46; 26pp; English.  
 PS This is the amino acid sequence of soybean stearyl ACP-desaturase,  
 CC used in the method of the invention, which involves the creation of  
 CC chimeric genes which are used in (antisense orientation) to transform  
 CC plant cells. The nucleic acids are useful for controlling the levels  
 CC of (unsaturated fatty acids in soybean oil. In transformed cells  
 CC (seeds), the chimeric genes transcribe the antisense RNA to the  
 CC complementary mRNA for the enzyme. This results in inhibition of  
 CC expression of the endogenous enzyme and reduction in desaturation of  
 CC seed oil. This results in seed oil which is low in saturates and  
 CC polyunsaturates and high in monosaturates, giving an oil which is  
 CC healthier.  
 XX Sequence 391 AA;  
 SQ

Query Match 91.5%; Score 1753; DB 19; Length 391;  
 Best Local Similarity 89.8%; Pred. No. 2.9e-156;  
 Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

QY 1 ASTLKSKEVENLKPPFPPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60  
 DB 29 ASTLRSGSKEVENIKKPPFTPPREVHVQVTHSMPPQKIEIFKSLDNWADQNILTHLKPVEK 88  
 QY 61 CWPQDFLPDPASDGDGDEQVRELRAKEIPDDYFVVLVGDMMITEALPYQTMNLTLG 120  
 DB 89 CWPQDFLPDPSSDGDGFEQVKELRAKEIPDDYFVVLVGDMMITEALPYQTMNLTLG 148  
 QY 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180  
 DB 149 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 208  
 QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGMIASDEKRHETATYKIV 240  
 DB 209 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGMIASDEKRHETATYKIV 268  
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAQRGLGYTAKDYADI 300  
 DB 269 EKLFEVDPDGTVMAFADMMRKKIKAMPAHLMYDGRDDNLFDFNYSVAQRIGVYTAQDYADI 328  
 QY 301 LEFLVGRWKVDKLTGLSAGOKAQDYVCRLLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 360  
 DB 329 LEFLVGRWKVEQLTGLSGEGRKAQYVCGLPPIRRLEERAQRAKESSTLKFWSWIHDRE 388  
 QY 361 VKL 363  
 DB 389 VLL 391

RESULT 6  
 AAR14188  
 ID AAR14188 standard; Protein; 396 AA.  
 AC AAR14188;  
 XX 11-DEC-1991 (first entry)  
 DT C. tinctorius delta9 desaturase from pcgn274.  
 DE Desaturase; fatty acid; saturation; chill tolerance; lipid;  
 KW herbicide.  
 KW Carthamus tinctorius.  
 OS  
 XX Key Location/Qualifiers  
 FT Peptide 1..33  
 FT /label= transit\_peptide  
 FT Protein 34..396  
 FT /label= mature\_protein  
 XX WO9113972-A.  
 PN  
 XX

PD 19-SEP-1991.  
XX  
PF 14-MAR-1991; 91WO-U001746.  
XX  
XX 14-NOV-1990; 90US-0615784.  
PR 16-MAR-1990; 90US-0494106.  
XX 13-AUG-1990; 90US-0567373.  
XX  
PA (CALG-) CALGENE INC.  
XX  
XX Thompson G, Knauf V;  
XX  
XX WPI; 1991-295627/40.  
DR N-PSDB; AAQ13963.  
XX  
XX DNA encoding a plant desaturase - used for modifying the satd.  
PT fatty acid compsn. of plant cells and plant seeds  
XX  
XX Disclosure; Fig 2; 128pp; English.  
XX  
CC Modification of fatty acid in a plant host cell to a different  
CC percentage of fatty acid satn. is possible by growing a host plant  
CC cell having integrated into its genome a recombinant DNA sequence  
CC encoding this protein, under the control of regulatory elements  
CC functional in the plant cell during lipid accumulation, under  
CC conditions which will promote the activity of the regulatory elements.  
CC By increasing the amt. of desaturase available in plant cells, an  
CC increased percentage of unsatd. fatty acids may be provided, using  
CC anti-sense technology, the amt. of desaturase can be decreased,  
CC resulting in a higher percentage of fatty acids.  
CC Using the desaturase gene and derivs. in cells and plants,  
CC desirable traits such as chill tolerance may be introduced and  
CC environmentally safe herbicide prods. may be provided.  
CC See also AAQ13963-69.  
XX  
SQ Sequence 396 AA;  
Query Match 91.4%; Score 1752; DB 12; Length 396;  
Best Local Similarity 90.1%; Pred. No. 3.7e-156;  
Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;  
QY 1 ASTLGSKEVENLKKPFMPREHVQVTHSMPPQKIEIFKSLDNNAENILVHLKPVEK 60  
DB 34 ASTLGSSTPKVDNAKKFPQPPREHVQVTHSMPPQKIEIFKSLDNNAENILVHLKPVEK 93  
QY 61 CWOQDFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120  
DB 94 CWOAQDFLPDPASEGDFEQVKELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153  
QY 121 VRDETGAPTSNAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180  
DB 154 VRDETGASLTPAWVWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 213  
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADKRHETATYTKIV 240  
DB 214 TENSPLYGFIYTSFQERATFVSHGNTARHAKDHGVKLAQICGTIASDEKREHETATYTKIV 273  
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRLGVYTKADYADI 300  
DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRLGVYTKADYADI 333  
QY 361 VKL 363  
DB 394 VKL 396  
RESULT 7  
AAR22048  
ID AAR22048 standard; Protein; 396 AA.

XX AAR22048;  
AC  
XX 07-JUL-1992 (first entry)  
DT  
XX Carthamus tinctorius desaturase.  
DE  
XX Safflower; fatty acid synthesis; seed; acyl carrier protein;  
KW lipids.  
XX  
XX Carthamus tinctorius.  
OS  
XX W09203564-A.  
PN  
XX 05-MAR-1992.  
PD  
XX 15-AUG-1991; 91WO-U005801.  
PF  
XX 26-JUN-1991; 91US-0721761.  
PR 15-AUG-1990; 90US-0568493.  
XX  
XX (CALG-) CALGENE INC.  
PA  
XX Knauf VC, Thompson GA;  
PI  
XX WPI; 1992-096907/12.  
DR N-PSDB; AAQ22616.  
XX  
XX New plant beta-keto:acyl synthase protein - obtd. from Ricinus  
PT communis, useful e.g. for modifying fatty acid compsn.  
XX  
XX Disclosure; Fig 8; 157pp; English.  
XX  
CC The protein sequence was deduced from the desaturase gene isolated  
CC from Carthamus tinctorius as the clone pCGN2754. The clone can be  
CC used to construct acyl carrier protein expression cassettes in a  
CC binary vector for plant transformation. This allows integration  
CC of nucleic acids encoding a desaturase sequence and a synthase  
CC sequence into the genome of a host cell. A plant desaturase  
CC includes any enzyme capable of catalysing the insertion of a first  
CC double bond into a fatty acid-ACP moiety especially between C9-C10.  
CC See also AAR22046-53.  
XX  
SQ Sequence 396 AA;  
Query Match 91.4%; Score 1752; DB 13; Length 396;  
Best Local Similarity 90.1%; Pred. No. 3.7e-156;  
Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;  
QY 1 ASTLGSKEVENLKKPFMPREHVQVTHSMPPQKIEIFKSLDNNAENILVHLKPVEK 60  
DB 34 ASTLGSSTPKVDNAKKFPQPPREHVQVTHSMPPQKIEIFKSLDNNAENILVHLKPVEK 93  
QY 61 CWOQDFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120  
DB 94 CWOAQDFLPDPASEGDFEQVKELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153  
QY 121 VRDETGAPTSNAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180  
DB 154 VRDETGASLTPAWVWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 213  
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADKRHETATYTKIV 240  
DB 214 TENSPLYGFIYTSFQERATFVSHGNTARHAKDHGVKLAQICGTIASDEKREHETATYTKIV 273  
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRLGVYTKADYADI 300  
DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRLGVYTKADYADI 333  
QY 301 LEFLVGRWKVKDLTGLSAGCAQDYVCGLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 360  
DB 334 LEFLVGRWKVKDLTGLSAGCAQDYVCGLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 393

QY 361 VKL 363  
 DB 394 VKL 396  
 RESULT 8  
 AAR54033  
 ID AAR54033 standard; Protein; 396 AA.  
 XX  
 AC AAR54033;  
 XX  
 DT 01-DEC-1994 (first entry)  
 XX  
 DE Sequence encoding desaturase enzyme.  
 XX  
 KW Synthase; plants; oil; seed; fatty acids; gene expression;  
 KW biosynthesis; ss.  
 XX  
 OS C. tinctorius.  
 XX  
 PN WO9410189-A.  
 XX  
 PD 11-MAY-1994.  
 XX  
 PF 02-NOV-1993; 93WO-US10526.  
 XX  
 PR 02-NOV-1992; 92US-0971182.  
 XX  
 PA (CALJ ) CALGENE INC.  
 XX  
 PI Knaf VC, Thompson GA;  
 XX  
 DR WPI: 1994-167378/20.  
 DR N-PSDB; AAQ64003.  
 XX  
 FT DNA constructs encoding beta-keto:acyl-ACP synthase - useful to  
 PT modify the oil content of seeds, e.g. for dietary purposes  
 XX  
 PS Disclosure; Figure 10; 85pp; English.  
 XX  
 CC Higher plants appear to share a common metabolic pathway for the  
 CC synthesis of fatty acids. Genes encoding synthase proteins may be  
 CC used in nucleic acid constructs to modulate the amount of synthase  
 CC activity in a host cell. Nucleic acid constructs may also be  
 CC designed to decrease the expression of a synthase protein, i.e.,  
 CC constructs containing anti-sense synthase sequences. The constructs  
 CC allow the generation of plants bearing seeds which have enhanced oil  
 CC yields and/or altered compositions of oils. The production of  
 CC common plant unsaturated fatty acids is catalysed by a desaturase.  
 CC Oleic, linoleic and alpha-linoleic acids found in storage  
 CC triglycerides are produced from the desaturation of stearoyl-ACP to  
 CC form oleoyl-ACP.  
 XX  
 SQ Sequence 396 AA;

Query Match 91.4%; Score 1752; DB 15; Length 396;  
 Best Local Similarity 90.1%; Pred. No. 3.7e-156;  
 Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 ASTLKSKEVENLKKPFMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVKE 60  
 DB 34 ASTLGSSTPKVDNAKKFPQPPREVHVQVTHSMPPQKIEFKSGEWAQNLVHLKPVKE 93  
 QY 61 CWOQDFLPDASGDFEQVRELREARKEIPDDYFVLVGDMITTEALPTYQTMLNTLDG 120  
 DB 94 CWOQDFLPDASEGDFEQVRELREARKEIPDDYFVLVGDMITTEALPTYQTMLNTLDG 153  
 QY 121 VDETGAFTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQTEKTIQYLGSGMDPR 180  
 DB 154 VDETGAFTSWAVWTRAWTAENRHGDLNKKLYLSGRVDMRQTEKTIQYLGSGMDPR 213  
 QY 181 TENSPLYLGFYTSFQERATFVSHGNTARHAKDHGDKVLAQICGTIASDEKRHETAYTKIV 240

DB 214 TENSPLYLGFYTSFQERATFVSHGNTARHAKDHGDKVLAQICGTIASDEKRHETAYTKIV 273  
 QY 241 EKLFEIDPDGTVLAFADMRKKISMPAHLMYDGRDDNLFDFHESAVAQRLGVYTAQDYADI 300  
 DB 274 EKLFEIDPDGTVLAFADMRKKISMPAHLMYDGRDDNLFDFHESAVAQRLGVYTAQDYADI 333  
 QY 301 LEFLVGRWKVDKLTGLSAEGOKAQDYVCRLLPPRIIRLLEERAQGRAKEAPTMPFSWIFDRQ 360  
 DB 334 LEFLVGRWKVADLTGLSGEGKQADYVCGLLPPRIIRLLEERAQGRAKEGVPVFPFSWIFDRQ 393  
 QY 361 VKL 363  
 DB 394 VKL 396  
 RESULT 9  
 AAW44349  
 ID AAW44349 standard; Protein; 396 AA.  
 XX  
 AC AAW44349;  
 XX  
 DT 28-MAY-1998 (first entry)  
 XX  
 DE Carthamus tinctorius desaturase from clone pCGN2754.  
 XX  
 KW Carthamus tinctorius; safflower; delta-9 desaturase; oilseed;  
 KW fatty acid saturation.  
 XX  
 OS Carthamus tinctorius.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..33  
 FT FT /label= signal  
 FT Protein 34..396  
 FT FT /label= desaturase  
 XX  
 PN US5723595-A.  
 XX  
 PD 03-MAR-1998.  
 XX  
 PF 06-JUN-1995; 95US-0471791.  
 XX  
 PR 16-SEP-1991; 91US-0762762.  
 PR 16-MAR-1990; 90US-0494106.  
 PR 13-AUG-1990; 90US-0567373.  
 PR 14-NOV-1990; 90US-0615784.  
 PR 14-MAR-1991; 91WO-US01746.  
 PR 06-JUN-1995; 95US-0471791.  
 XX  
 PA (CALJ ) CALGENE INC.  
 XX  
 PI Knaf VC, Thompson GA;  
 XX  
 DR WPI: 1998-178544/16.  
 DR N-PSDB; AAV15250.  
 XX  
 PT DNA encoding plant delta-9 desaturase protein - having amino acid  
 PT sequence of Carthamus tinctorius desaturase, useful for, e.g.  
 PT producing oil-seeds with modified levels of fatty acid saturation  
 XX  
 PS Claim 5; Column 53-56; 87pp; English.  
 XX  
 CC The present sequence represents a Carthamus tinctorius desaturase from  
 CC clone pCGN2754. The present invention describes a recombinant DNA  
 CC construct comprising a DNA sequence encoding a plant delta-9 desaturase  
 CC protein. The present invention also provides a method of modifying fatty  
 CC acid composition in a host plant cell from a given fatty acid saturation  
 CC to a different fatty acid saturation, comprising growing a host plant  
 CC cell containing a recombinant DNA sequence which encodes a plant  
 CC desaturase under the control of regulatory elements functional in the  
 CC plant cell during lipid accumulation. Also, oilseeds having a modified  
 CC level of fatty acid saturation and oils produced from such oilseeds.



30-APR-1999;	99US-0132407;
PR 04-MAY-1999;	99US-0132484;
PR 05-MAY-1999;	99US-0132485;
PR 06-MAY-1999;	99US-0132486;
PR 06-MAY-1999;	99US-0132487;
PR 07-MAY-1999;	99US-0132863;
PR 11-MAY-1999;	99US-0134256;
PR 14-MAY-1999;	99US-0134218;
PR 14-MAY-1999;	99US-0134219;
PR 14-MAY-1999;	99US-0134370;
PR 18-MAY-1999;	99US-0134768;
PR 19-MAY-1999;	99US-0134941;
PR 20-MAY-1999;	99US-0135124;
PR 21-MAY-1999;	99US-0135353;
PR 24-MAY-1999;	99US-0135629;
PR 25-MAY-1999;	99US-0136021;
PR 27-MAY-1999;	99US-0136392;
PR 28-MAY-1999;	99US-0136783;
PR 01-JUN-1999;	99US-0137222;
PR 03-JUN-1999;	99US-0137528;
PR 04-JUN-1999;	99US-0137502;
PR 07-JUN-1999;	99US-0137724;
PR 08-JUN-1999;	99US-0138094;
PR 10-JUN-1999;	99US-0138540;
PR 10-JUN-1999;	99US-0138847;
PR 14-JUN-1999;	99US-0139119;
PR 16-JUN-1999;	99US-0139452;
PR 16-JUN-1999;	99US-0139453;
PR 17-JUN-1999;	99US-0139492;
PR 18-JUN-1999;	99US-0139454;
PR 18-JUN-1999;	99US-0139455;
PR 18-JUN-1999;	99US-0139456;
PR 18-JUN-1999;	99US-0139457;
PR 18-JUN-1999;	99US-0139458;
PR 18-JUN-1999;	99US-0139459;
PR 18-JUN-1999;	99US-0139460;
PR 18-JUN-1999;	99US-0139461;
PR 18-JUN-1999;	99US-0139462;
PR 18-JUN-1999;	99US-0139463;
PR 18-JUN-1999;	99US-0139750;
PR 18-JUN-1999;	99US-0139763;
PR 21-JUN-1999;	99US-0139817;
PR 22-JUN-1999;	99US-0139899;
PR 23-JUN-1999;	99US-0140353;
PR 23-JUN-1999;	99US-0140354;
PR 24-JUN-1999;	99US-0140695;
PR 28-JUN-1999;	99US-0140823;
PR 29-JUN-1999;	99US-0140991;
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PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
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PR 23-SEP-1999; 99US-0155486.  
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PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
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PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 90.4%; Score 1733; DB 21; Length 401;  
Best Local Similarity 89.4%; Pred. No. 2.3e-154;  
Matches 322; Conservative 22; Mismatches 16; Indels 0; Gaps 0;

QY 4 LKSGSKEVENLKKPFMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKQW 63  
DB 42 LSSGPKVEVESLKKPFTPPREHVQVHLHSMPPQKIEIFKSMENWAEENLLIHLKDVESQW 101  
QY 64 PQDFLPDPASDGEQVRELRAKEIPDDYFVVLVGDITEEALPTYQTMNLTDGVRD 123  
DB 102 PQDFLPDPASDGEQVRELRAKEIPDDYFVVLVGDITEEALPTYQTMNLTDGVRD 161  
QY 124 ETGASPTSWAITWTRAMTAENRHGDLNLYLSGRVDMRQIEKTIQYLLIGSGMDPRTEN 183  
DB 162 ETGASPTSWAITWTRAMTAENRHGDLNLYLSGRVDMRQIEKTIQYLLIGSGMDPRTEN 221  
QY 184 SPYLGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRKHETAYTKIVEKL 243  
DB 222 NPYLGFYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRKHETAYTKIVEKL 281  
QY 244 FEIDPDGTVLAFADMMRKKTSMFAHLMYDGRDNDNLFDFHSAVQRLGVYTKADYADILEF 303  
DB 282 FEIDPDGTVMFAFADMMRKKTSMFAHLMYDGRDNDNLFDFHSAVQRLGVYTKADYADILEF 341  
QY 304 LVGRWKVDKLTGLTSAEGOKAQDYVCRPLPRIRLEERAQAKRAKEAPTMFESWIFEDROVKL 363  
DB 342 LVGRWKIQDLTGLSGEGNKAQDYLCGLAPRIKRLDERAQARAKKGPKIPFESWIHREVQL 401

RESULT 11  
ABB92108  
ID ABB92108 standard; Protein; 401 AA.  
XX  
AC ABB92108;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Herbicidally active polypeptide SEQ ID NO 1319.  
XX  
KW Herbicidal; plant; agriculture; herbicide.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200210210-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 28-AUG-2001; 2001WO-EF09892.  
XX  
PR 28-AUG-2001; 2001WO-EF09892.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Tietjen K, Weidler M;



89	CWQPDQFLPNPSSDGE	EEQVKLE	RRKAKEITLTYFFVVLV	GDMLTEALPTYQTMLNTLDG	14		
QY	121	VROETGASPTSWAIWTRAWTA	AEENRHGDLN	KLYLSGRVDMRQ	IEKTIQYLLIGSGMDPR	180	
DB	149	VROETGASLTWAIWTRAWTA	AEENRRHGDLLN	KLYLSGRVDMKQ	IEKTIQYLLIGSGMDPR	208	
QY	181	TENSPYLGFYTSFQERATP	ISHGNTARQAK	EHGDIKLAQICGT	IAADEKRRHETATKIV	240	
DB	209	TENSPYLGFYTSFQERATP	ISHGNTARLAK	EHGDIKLAQICGMIAS	DEKRRHETATKIV	268	
QY	241	EKLFEDPDGCTVLAFA	ADMRRKKISM	PAHLMYDGRDNL	DFHFSAVAQR	LVGVYTA	300
DB	269	EKLFEDVDGCTVAFAD	MMRRKKIAMP	PAHLMYDGRDNL	DFNYSAVAQR	IGVYTA	328
QY	301	LEFLVGRWKVKDTGLT	LSAEGOKAQDY	VCRLPPRIR	RLLEERAQGR	AKEAPT	360
DB	329	LEFLVGRWKVEQTLG	LSGEGRKAQY	VCGLPPRIR	RLLEERAQGR	KESSTL	388
QY	361	VKL	363				
DB	389	VLL	391				
RESULT 14							
AAR14190							
ID	AAR14190 standard; Protein; 398 AA.						
XX	AAR14190;						
AC							
DT	11-DEC-1991 (first entry)						
XX	B. campestris delta9 desaturase from PCGN3235.						
DE	Desaturase; fatty acid; saturation; chill tolerance; lipid;						
KW	herbicide.						
OS	Brassica campestris.						
XX							
PN	WO9113972-A.						
XX	19-SEP-1991.						
XX	14-MAR-1991; 91WO-U001746.						
PF							
PR	14-NOV-1990; 90US-0615784.						
PR	16-MAR-1990; 90US-0494106.						
PR	13-AUG-1990; 90US-0567373.						
XX	(CALG-) CALGENE INC.						
PA							
PI	Thompson G, Knauf V;						
XX							
DR	WPI; 1991-295627/40.						
DR	N-PSDB; AAQ13965.						
XX							
PT	DNA encoding a plant desaturase - used for modifying the satd.						
XX	fatty acid compsn. of plant cells and plant seeds						
PS	Disclosure; Fig 4C; 128pp; English.						
XX							
CC	Modification of fatty acid in a plant host cell to a different						
CC	percentage of fatty acid satn. is possible by growing a host plant						
CC	cell having integrated into its genome a recombinant DNA sequence						
CC	encoding this protein, under the control of regulatory elements						
CC	functional in the plant cell during lipid accumulation, under						
CC	conditions which will promote the activity of the regulatory elements						
CC	By increasing the amt. of desaturase available in plant cells, an						
CC	increased percentage of unsatd. fatty acids may be provided, using						
CC	anti-sense technology, the amt. of desaturase can be decreased,						
CC	resulting in a higher percentage of fatty acids.						
CC	using the desaturase gene and derivs. in cells and plants,						
CC	desirable traits such as chill tolerance may be introduced and						
CC	environmentally safe herbicide prods. may be provided.						

CC See also AAQ13963-69.

XX SQ Sequence 398 AA;

Query Match 88.6%; Score 1698; DB 12; Length 398;  
Best Local Similarity 88.2%; Pred. No. 4.5e-151;  
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 8 SKEVENLKKPPMPREVHVQVTHSPPKIEIFKSLDNWAEENILVHLKPVCKWQPODF 67  
DB 43 SKEVESLKKPFTPPKEVHVQVHLHSMPPKIEIFKSWEDWAGNLTQLKDKVEKSWQPODF 102  
QY 68 LPDPASDGFDEQVRELREAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDGVRDETGA 127  
DB 103 LPDPASDGFDEQVRELREARERELPDDYFVVLVGDMMITEALPTYQTMNTLDGVRDETGA 162  
QY 126 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTENSPYL 187  
DB 163 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTENSPYL 222  
QY 188 GFITYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIVEKLFELD 247  
DB 223 GFITYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIVEKLFELD 282  
QY 248 PDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSVAQAQRLGVVYAKDYADILEFLVGR 307  
DB 283 PDGTVMAFADMMRKKISMPAHLMYDGRDESLEDFNFSVAQRLGVVYAKDYADILEFLVGR 342  
QY 308 WKVDKLTGLSAGGQKAQDYVCRLLPPIRLLEERAQRAKEAPTMPFSWIFDROVKL 363  
DB 343 WKIESLTGLSGEGNKAQYELCGLTPRIIRLDERAQAARAKKGPVPFSWIHDREVQL 398

#### RESULT 15

AAW14798

ID AAW14798 standard; Protein; 398 AA.

XX AC AAW14798;

XX DT 03-JUL-1997 (first entry)

XX DE Rapeseed stearyl-ACP desaturase BND9.

XX KW Stearyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;  
XX KW antisenase; triglyceride; stearic acid; transgenic plant; oilseed;  
XX KW vegetable oil; mangosteen; Garcinia mangifera.

XX OS Brassica napus cv. 212/86.

XX PN WO9712047-A1.

XX PD 03-APR-1997.

XX PF 30-SEP-1996; 96WO-US16078.

XX PR 29-SEP-1995; 95US-0537083.

XX PA (CALJ ) CALGENE INC.

XX PI Knauf VC, Kridl J, Lassner MW;

XX DR WPI; 1997-212906/19.

XX DR N-PSDB; AAT63438.

XX PT Increasing levels of stearate in plant seed triglyceride(s)  
XX PT using a DNA sequence encoding acyl-ACP thioesterase protein having  
XX PT substantial activity on C18:0 acyl-ACP substrates

XX PS Example 5; Fig7A-7C; 55pp; English.

XX CC Oilseed rape stearyl-ACP desaturases BND11 (AAW14797) and BND9  
XX CC (AAW14798) each catalyse the desaturation of stearyl-ACP (C18:0) to  
XX CC oleoyl-ACP (C18:1). Their amino acid sequences were deduced from

CC cDNA clones (AAT63437-38) isolated from a Brassica napus cv. 212/86  
CC mid-mutation seed cDNA library. An antisense gene was constructed  
CC to generate antisense RNA homologous to both BND9 and BND11. In  
CC transgenic Brassica plants expressing the stearyl-ACP desaturase  
CC antisense construct and mangosteen Class I acyl-ACP thioesterase  
CC GarmFAT1 (see also AAW14795), levels of C18:0 in the seed oil may  
CC exceed 50% of total fatty acids.

XX SQ Sequence 398 AA;

Query Match 88.6%; Score 1698; DB 18; Length 398;  
Best Local Similarity 88.2%; Pred. No. 4.5e-151;  
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 8 SKEVENLKKPPMPREVHVQVTHSPPKIEIFKSLDNWAEENILVHLKPVCKWQPODF 67  
DB 43 SKEVESLKKPFTPPKEVHVQVHLHSMPPKIEIFKSWEDWAGNLTQLKDKVEKSWQPODF 102  
QY 68 LPDPASDGFDEQVRELREAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDGVRDETGA 127  
DB 103 LPDPASDGFDEQVRELREARERELPDDYFVVLVGDMMITEALPTYQTMNTLDGVRDETGA 162  
QY 128 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTENSPYL 187  
DB 163 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTENSPYL 222  
QY 188 GFITYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIVEKLFELD 247  
DB 223 GFITYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIVEKLFELD 282  
QY 248 PDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSVAQAQRLGVVYAKDYADILEFLVGR 307  
DB 283 PDGTVMAFADMMRKKISMPAHLMYDGRDESLEDFNFSVAQRLGVVYAKDYADILEFLVGR 342  
QY 308 WKVDKLTGLSAGGQKAQDYVCRLLPPIRLLEERAQRAKEAPTMPFSWIFDROVKL 363  
DB 343 WKIESLTGLSGEGNKAQYELCGLTPRIIRLDERAQAARAKKGPVPFSWIHDREVQL 398

Search completed: March 7, 2003, 03:08:44

Job time : 41 secs

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